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OM protein - protein search, using sw model

Run on: July 15, 2002, 12:46:44 ; Search time 29.22 seconds
(without alignments)
95.032 Million cell updates/sec

Title: US-09-938-700-4
Perfect score: 136
Sequence: 1 CRVTHPLPKDIVSIKAPCKRAP 25

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 253524

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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2: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT:*
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21: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | ID | Description |
|------------|-------|--------------------|----|-------------|
| 1 | 102 | 75.0 | 20 | AAW24102 |
| 2 | 89 | 65.4 | 17 | AAV50893 |
| 3 | 89 | 65.4 | 17 | AAV50894 |
| 4 | 89 | 65.4 | 25 | AAV79999 |
| 5 | 79 | 58.1 | 20 | AAW24103 |
| 6 | 72 | 52.9 | 17 | AAV50895 |
| 7 | 69 | 50.7 | 17 | AAV50895 |
| 8 | 68 | 50.0 | 25 | AAI80085 |
| 9 | 65 | 47.8 | 17 | AAI80080 |
| 10 | 64 | 47.1 | 25 | AAV79998 |
| 11 | 64 | 47.1 | 25 | AAV91212 |

| | | | | |
|----|----|------|----|-----------|
| 12 | 64 | 47.1 | 25 | AAI68602 |
| 13 | 63 | 46.3 | 25 | AAV80077 |
| 14 | 61 | 44.9 | 17 | AAV50897 |
| 15 | 60 | 44.1 | 22 | AAV42585 |
| 16 | 60 | 44.1 | 24 | AAV42586 |
| 17 | 57 | 41.9 | 17 | AAV802179 |
| 18 | 55 | 40.4 | 19 | AAI68503 |
| 19 | 55 | 40.4 | 19 | AAI68300 |
| 20 | 55 | 40.4 | 19 | AAI68103 |
| 21 | 51 | 37.5 | 13 | AAI68518 |
| 22 | 51 | 37.5 | 13 | AAI6849 |
| 23 | 46 | 33.8 | 25 | AAV80048 |
| 24 | 44 | 32.4 | 20 | AAI68001 |
| 25 | 44 | 32.4 | 20 | AAV58439 |
| 26 | 44 | 32.4 | 20 | AAV70931 |
| 27 | 44 | 32.4 | 20 | AAI68121 |
| 28 | 42 | 30.9 | 12 | AAI68517 |
| 29 | 42 | 30.9 | 12 | AAI6848 |
| 30 | 42 | 30.9 | 16 | AAV50900 |
| 31 | 41 | 30.1 | 25 | AAV80001 |
| 32 | 40 | 29.4 | 15 | AAV50899 |
| 33 | 39 | 28.7 | 9 | AAV69599 |
| 34 | 39 | 28.7 | 9 | AAV69600 |
| 35 | 39 | 28.7 | 9 | AAV50891 |
| 36 | 39 | 28.7 | 9 | AAV50892 |
| 37 | 39 | 28.7 | 14 | AAV69579 |
| 38 | 38 | 27.9 | 14 | AAI68519 |
| 39 | 38 | 27.9 | 14 | AAI6850 |
| 40 | 38 | 27.9 | 22 | AAI6850 |
| 41 | 38 | 27.9 | 22 | AAI6850 |
| 42 | 37 | 27.2 | 12 | AAI68516 |
| 43 | 37 | 27.2 | 12 | AAI6847 |
| 44 | 37 | 27.2 | 12 | AAI6847 |
| 45 | 36 | 26.5 | 14 | AAV00560 |

ALIGNMENTS

| | | |
|----------|--|---------------------------|
| RESULT 1 | AAW24102 | standard; peptide: 20 AA. |
| XX | AAW24102; | |
| AC | 21-NOV-1997 (first entry) | |
| DT | Canine immunoglobulin E peptide 5. | |
| DE | Immunoglobulin E; Ige; anti-canine Ige antibody; allergy; canine; dog. | |
| KW | Canis familiaris. | |
| OS | JP09169795-A. | |
| PN | 30-JUN-1997. | |
| XX | 22-DEC-1995; 95JP-0334381. | |
| XX | 22-DEC-1995; 95JP-0334381. | |
| XX | (HITB) HITACHI CHEM CO LTD. | |
| PA | WPI: 1997-389423/36. | |
| XX | N-PSDB; AAT85651. | |
| DR | Canine immunoglobulin E peptide fragment and related DNA - useful for the preparation of anti-canine immunoglobulin E antibody | |
| PT | Claim 2; Page 9; 12pp; Japanese. | |
| XX | AAW24098-106 are peptide fragments containing at least 5 continuous amino acids of the partial canine immunoglobulin E (Ige) protein shown | |
| PS | | |
| XX | | |
| CC | | |

Peptide sequence o
Optimised Ige-CH3
Antibody 15A.2 bin
Ige peptide antago
Ige peptide antago
Ige peptide antago
Peptide which bind
Human Ige C epsilon
Peptide P7A derive
Ige peptide #11.
Human Ige C epsilon
Peptide P13b deriv
Ige derived target
Peptide #5328 enco
Human brain expres
Human bone marrow
Peptide #5258 enco
Human Ige C epsilon
Peptide P13a deriv
Antibody 15A.2 equ
Optimised Ige-CH3
Antibody 15A.2 mur
Monoclonal antibod
Antibody 15A.2 bin
Antibody 15A.2 bin
Immunogenic peptid
Human Ige C epsilon
Peptide P13c deriv
Peptide #4 having
Novel human diagno
Human Ige C epsilon
Peptide P13 deriv
Ige peptide #16.
Human protein frag

CC In AAW24097. The peptides are used for the preparation of anti-canine
CC IgE antibody. The anti-canine IgE antibody can be used for the diagnosis
CC of canine allergies.
XX
SQ Sequence 20 AA;

Query Match 75.0%; Score 102; DB 18; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.1e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CRTVHPHPKDIVRSIAKA 19
| | | | | | | | | | | | | | | | | | | | | |
DB 2 CRTVHPHPKDIVRSIAKA 20

RESULT 2

AAV50893
ID AAV50893 standard; peptide; 17 AA.

AC AAV50893;

DT 24-FEB-2000 (first entry)

DE Antibody 15A.2 binding peptide 10 from Phoc7c phage display library.

KW Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy;

KM epitope; prophylaxis; treatment; mimotope.

OS Synthetic.

PN EP957111-A2.

PD 17-NOV-1999.

PF 09-APR-1999; 99EP-0107035.

PR 09-APR-1998; 98US-0058331.

PR 30-MAR-1999; 99US-0281760.

PA (IDEX-) IDEXX LAB INC.

PI Lawton R, Mermet B, Francoeur G;

DR WPI; 2000-040833/04.

Binding proteins used for treatment or prophylaxis of canine allergy -

PS Disclosure; Fig 6; 30pp; English.

CC This invention describes a novel binding protein which specifically
CC binds to native canine free or B-cell bound IgE, and which doesn't bind
CC to IgE when the IgE is bound to mast cells. The peptide products of the
CC invention have anti-allergic activity. The antibodies bind to defined
CC epitopes on free or B-cell bound IgE molecules which have an important
CC role in allergic reaction. The specific binding proteins are used to
CC produce a pharmaceutical composition, preferably with a diluent, which
CC can be used for prophylaxis or treatment of canine allergy.
CC AAV50876-Y50900 represent peptide mimotopes used in the method of the
CC invention.
XX
SQ Sequence 17 AA;

Query Match 65.4%; Score 89; DB 21; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CRTVHPHPKDIVRSI 16
| | | | | | | | | | | | | | | | | |
DB 2 CRTVHPHPKDIVRSI 17

RESULT 3
AAV50894
ID AAV50894 standard; peptide; 17 AA.

AC AAV50894;

DT 24-FEB-2000 (first entry)

DE Antibody 15A.2 canine IgE binding epitope 1.

KW Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy;

KM epitope; prophylaxis; treatment; mimotope.

OS Synthetic.

PN EP957111-A2.

PD 17-NOV-1999.

PF 09-APR-1999; 99EP-0107035.

PR 09-APR-1998; 98US-0058331.

PR 30-MAR-1999; 99US-0281760.

PA (IDEX-) IDEXX LAB INC.

PI Lawton R, Mermet B, Francoeur G;

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Binding proteins used for treatment or prophylaxis of canine allergy -

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CC This invention describes a novel binding protein which specifically
CC binds to native canine free or B-cell bound IgE, and which doesn't bind
CC to IgE when the IgE is bound to mast cells. The peptide products of the
CC invention have anti-allergic activity. The antibodies bind to defined
CC epitopes on free or B-cell bound IgE molecules which have an important
CC role in allergic reaction. The specific binding proteins are used to
CC produce a pharmaceutical composition, preferably with a diluent, which
CC can be used for prophylaxis or treatment of canine allergy.
CC AAV50876-Y50900 represent peptide mimotopes used in the method of the
CC invention.
XX
SQ Sequence 17 AA;

Query Match 65.4%; Score 89; DB 21; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CRTVHPHPKDIVRSI 16
| | | | | | | | | | | | | | | | | |
DB 2 CRTVHPHPKDIVRSI 17

RESULT 4

AAV79999
ID AAV79999 standard; Peptide; 25 AA.

AC AAV79999;

DT 15-MAY-2000 (first entry)

DE Optimised IgE-CH3 domain antigen peptide for dog IgE.

KW Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
KW antibody; allergy; allergic disease; immunisation; anti-allergic;
KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
OS Canis sp.

OS Synthetic.

XX
PN WO9967293-A1.
XX
PD 29-DEC-1999.
XX
PF 21-JUN-1999; 99WO-US13959.
XX
PR 20-JUN-1998; 98US-0100287.
XX

PA (UNBI-) UNITED BIOMEDICAL INC.

XX
PI Wang CY, Walfeld AM;
XX
DR WPI; 2000-160578/14.
XX

PT New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
XX for immunization against allergy.

PS Claim 1; Page 99; 155pp; English.

XX
CC The present invention describes immunoglobulin E (IgE)-CH3 domain
CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
CC and anti-asthmatic properties. (I) induces polyclonal antibodies
CC specific for a target effector site on the epsilon-heavy chain of IgE,
CC and so preventing triggering and activation of mast cells and basophils
CC and downregulation of IgE synthesis. Conjugates, or fusion peptides,
CC containing (I) are used for active immunisation against IgE-mediated
CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
CC dermatitis. Nucleic acids that encode these compounds are useful for
CC recombinant production of corresponding peptides or in DNA vaccines.
CC Conjugates of (I) that include a promiscuous T helper cell epitope
CC (functional in genetically diverse subjects), in addition to a B cell
CC target epitope, have increased immunogenicity and may include cyclic
CC constraints (disulfide bridge) to stabilise conformational features and
CC maximize cross-reactivity to the natural target. They induce safe
CC (non-anaphylactogenic) antibodies. AAY9994 to AAY0084 represent amino
CC acid sequences used in the exemplification of the present invention.
XX
SQ Sequence 25 AA;

Query Match 65.4%; Score 89; DB 21; Length 25;

Best Local Similarity 100.0%; Pred. NO. 8e-07;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 RVTGPHLPKDIVRSIAK 18
IIIIIIIIIIIIIIIIIIII
DB 8 rvtgphlpkdivrsiak 24

RESULT 5

AAW24103
ID AAW24103 standard; peptide; 20 AA.

XX
AC AAW24103;

XX
DT 21-NOV-1997 (first entry)

XX
DE Canine immunoglobulin E peptide 6.

XX
KM Immunoglobulin E; IgE; anti-canine IgE antibody; allergy; canine; dog.

XX
OS Canis familiaris.

XX
PN JP09169795-A.

XX
PD 30-JUN-1997.

XX
PF 22-DEC-1995; 95JP-0334381.

XX
PR 22-DEC-1995; 95JP-0334381.

PA (HITB) HITACHI CHEM CO LTD.

XX
DR WPI; 1997-389423/36.
XX
DR N-PSDB; AAT85652.

XX
PT Canine immunoglobulin E peptide fragment and related DNA - useful
XX for the preparation of anti-canine immunoglobulin E antibody

PS Claim 2; Page 9; 12pp; Japanese.

XX
CC AAW24098-106 are peptide fragments containing at least 5 continuous
CC amino acids of the partial canine immunoglobulin E (IgE) protein shown
CC in AAW24097. The peptides are used for the preparation of anti-canine
CC IgE antibody. The anti-canine IgE antibody can be used for the diagnosis
CC of canine allergies.
XX

SQ Sequence 20 AA;

Query Match 58.1%; Score 79; DB 18; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.2e-05;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 KDIVRSIAKAPKRAP 25
IIIIIIIIIIIIIIIIIIII
DB 1 kdivrsiakapkrap 16

RESULT 6

AAV50896
ID AAV50896 standard; peptide; 17 AA.

XX
AC AAV50896;

XX
DT 24-FEB-2000 (first entry)

XX
DE Antibody 15A.2 green monkey IgE binding epitope 1.

XX
KM Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy;

XX
KW epitope; prophylaxis; treatment; mimotope.

XX
OS Synthetic.

XX
PN EP957111-A2.

XX
PD 17-NOV-1999.

XX
PF 09-APR-1999; 99EP-0107035.

XX
PR 09-APR-1998; 98US-0058331.

XX
PR 30-MAR-1999; 99US-0281760.

XX
PA (IDEX-) IDEXX LAB INC.

XX
PI Lawton R, Mermer B, Francoeur G;

XX
DR WPI; 2000-040833/04.

XX
PT Binding proteins used for treatment or prophylaxis of canine allergy -

XX
PS Disclosure; Fig 7; 30pp; English.
XX
CC This invention describes a novel binding protein which specifically
CC binds to native canine free or B-cell bound IgE, and which doesn't bind
CC to IgE when the IgE is bound to mast cells. The peptide products of the
CC invention have anti-allergic activity. The antibodies bind to defined
CC epitopes on free or B-cell bound IgE molecules which have an important
CC role in allergic reaction. The specific binding proteins are used to
CC produce a pharmaceutical composition, preferably with a diluent, which
CC can be used for prophylaxis or treatment of canine allergy.
CC AAY50876-Y50900 represent peptide mimotopes used in the method of the
XX invention.

SQ Sequence 17 AA:

Query Match 52.9%; Score 72; DB 21; Length 17;
 Best Local Similarity 80.0%; Pred. No. 0.00022;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 CRVTHPLPKDIVRS 15
 |||||: |||
 DB 2 crvthplpralvrs 16

RESULT 7

AAV50895

ID AAV50895 standard; peptide; 17 AA.

XX AAV50895;

DT 24-FEB-2000 (first entry)

XX Antibody 15A.2 human IGE binding epitope 1.

XX Canine; allergy; antibody 15A.2; IGE; B cell; mast cell; anti-allergy;

KM epitope; prophylaxis; treatment; mimotope.

XX Synthetic.

XX EP957111-A2.

XX 17-NOV-1999.

XX 09-APR-1999; 99EP-0107035.

XX 09-APR-1998; 98US-0058331.

XX 30-MAR-1999; 99US-0281760.

XX (IDEX-) IDEXX LAB INC.

XX Lawton R, Mermer B, Francoeur G;

XX WPI; 2000-040833/04.

XX Binding proteins used for treatment or prophylaxis of canine allergy -

XX Disclosure; Fig 7; 30pp; English.

XX This invention describes a novel binding protein which specifically

XX binds to native canine free or B-cell bound IGE, and which doesn't bind

XX to IGE when the IGE is bound to mast cells. The peptide products of the

XX invention have anti-allergic activity. The antibodies bind to defined

XX epitopes on free or B-cell bound IGE molecules which have an important

XX role in allergic reaction. The specific binding proteins are used to

XX produce a pharmaceutical composition, preferably with a diluent, which

XX can be used for prophylaxis or treatment of canine allergy.

XX AAV50876-Y50900 represent peptide mimotopes used in the method of the

XX invention.

XX Sequence 17 AA:

Query Match 50.7%; Score 69; DB 21; Length 17;
 Best Local Similarity 73.3%; Pred. No. 0.00065;
 Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 CRVTHPLPKDIVRS 15
 |||||: |||
 DB 2 crvthplpralvrs 16

RESULT 8

AAV80000

ID AAV80000 standard; peptide; 25 AA.

XX AAV80000 standard; peptide; 25 AA.

AC AAV80000;

DT 15-MAY-2000 (first entry)

XX Optimised IGE-CH3 domain antigen peptide for rat IGE.

XX Immunoglobulin E; IGE; epsilon heavy chain; antigenic; antigen;

XX immunogenic; immunostimulatory; carrier protein; helper T cell epitope;

XX antibody; allergy; allergic disease; immunisation; anti-allergic;

XX anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

XX Rattus sp.

XX Synthetic.

XX WO967293-A1.

XX 29-DEC-1999.

XX 21-JUN-1999; 99WO-US13959.

XX 20-JUN-1998; 98US-0100287.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY, Walfield AM;

XX WPI; 2000-160578/14.

XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions

XX for immunization against allergy -

XX Claim 1; Page 99; 155pp; English.

XX The present invention describes immunoglobulin E (IGE)-CH3 domain

XX antigenic peptides (1). (1) have anti-allergic, anti-anaphylactic

XX and anti-asthmatic properties. (1) induces polyclonal antibodies

XX specific for a target effector site on the epsilon-heavy chain of IGE,

XX and so preventing triggering and activation of mast cells and basophils

XX containing (1) are used for active immunisation against IGE-mediated

XX allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy

XX dermatitis. Nucleic acids that encode these compounds are useful for

XX recombinant production of corresponding peptides or in DNA vaccines.

XX Conjugates of (1) that include a promiscuous T helper cell epitope

XX (functional in genetically diverse subjects), in addition to a B cell

XX target epitope, have increased immunogenicity and may include cyclic

XX constraints (disulfide bridge) to stabilise conformational features and

XX maximize cross-reactivity to the natural target. They induce safe

XX (non-anaphylactogenic) antibodies. AAV79994 to AAV80084 represent amino

XX acid sequences used in the exemplification of the present invention.

XX Sequence 25 AA:

Query Match 50.0%; Score 68; DB 21; Length 25;
 Best Local Similarity 76.5%; Pred. No. 0.0014;
 Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 RYTHPLPKDIVRSIAK 18
 |||||: |||||
 DB 8 ryvthplfpkdivrsitk 24

RESULT 9

AAV50898

ID AAV50898 standard; peptide; 17 AA.

XX AAV50898;

XX 24-FEB-2000 (first entry)

XX Antibody 15A.2 swine IGE binding epitope 1.

KM Canine; allergy; antibody 15A.2; IGE; B cell; mast cell; anti-allergy;
 KW epitope; prophylaxis; treatment; mimotope.

OS Synthetic.

PN EP957111-A2.

XX 17-NOV-1999.

XX 09-APR-1999; 99EP-0107035.

XX 09-APR-1998; 98US-0058331.

XX 30-MAR-1999; 99US-0281760.

XX (IDEX-) IDEX LAB INC.

XX Lawton R, Mermer B, Francoeur G;

XX WPI; 2000-040833/04.

XX Binding proteins used for treatment or prophylaxis of canine allergy -
 Disclosure; Fig 7; 30pp; English.

CC This invention describes a novel binding protein which specifically
 CC binds to native canine free or B cell bound IGE, and which doesn't bind
 CC to IGE when the IGE is bound to mast cells. The peptide products of the
 CC invention have anti-allergic activity. The antibodies bind to defined
 CC epitopes on free or B-cell bound IGE molecules which have an important
 CC role in allergic reaction. The specific binding proteins are used to
 CC produce a pharmaceutical composition, preferably with a diluent, which
 CC can be used for prophylaxis or treatment of canine allergy.
 CC AAY50876-Y50900 represent peptide mimotopes used in the method of the
 CC invention.

XX Sequence 17 AA;

Query Match 47.8%; Score 65; DB 21; Length 17;
 Best Local Similarity 75.0%; Pred. No. 0.0027;
 Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRVTHPLPKDIVRSI 16
 | | | | | | | | | | | | | | | | | |
 DB 2 CRVTHPLPKDIVRSI 17

RESULT 10

AAY79998
 ID AAY79998 standard; Peptide; 25 AA.

XX AAY79998;

XX 15-MAY-2000 (first entry)

DE Optimised IGE-CH3 domain antigen peptide for human IGE.

XX Immunoglobulin E; IGE; epsilon heavy chain; antigenic; antigen;
 KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
 KW antibody; allergy; allergic disease; immunisation; anti-allergic;
 KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

XX Homo sapiens.

OS Synthetic.

XX WO9967293-A1.

XX 29-DEC-1999.

XX 21-JUN-1999; 99WO-US13959.

XX 20-JUN-1998; 98US-0100287.

PA (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY, Walfield AM;

XX WPI; 2000-160578/14.

XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
 PT for immunization against allergy -

XX Claim 1; Page 21; 155pp; English.

CC The present invention describes immunoglobulin E (IGE)-CH3 domain
 CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
 CC and anti-asthmatic properties. (I) induces polyclonal antibodies
 CC specific for a target effector site on the epsilon-heavy chain of IGE,
 CC and so preventing triggering and activation of mast cells and basophils
 CC containing (I) are used for active immunisation against IGE-mediated
 CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
 CC dermatitis. Nucleic acids that encode these compounds are useful for
 CC recombinant production of corresponding peptides or in DNA vaccines.
 CC Conjugates of (I) that include a promiscuous T helper cell epitope
 CC (functional in genetically diverse subjects), in addition to a B cell
 CC target epitope, have increased immunogenicity and may include cyclic
 CC constraints (disulfide bridge) to stabilise conformational features and
 CC maximize cross-reactivity to the natural target. They induce safe
 CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino
 CC acid sequences used in the exemplification of the present invention.

XX Sequence 25 AA;

Query Match 47.1%; Score 64; DB 21; Length 25;
 Best Local Similarity 64.7%; Pred. No. 0.006;
 Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 RVTTHPLPKDIVRSIAR 18
 | | | | | | | | | | | | | | | | | |
 DB 8 RVTTHPLPKDIVRSIAR 24

RESULT 11

AAY91212
 ID AAY91212 standard; peptide; 25 AA.

XX AAY91212;

XX 22-MAY-2000 (first entry)

DE Modified human IGE CH3 domain, SEQ ID NO:92.

XX Promiscuous T-cell epitope; measles virus F protein; MVE;
 KW hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
 KW interleukin hormone releasing hormone; LRH; contraceptive; anticancer;
 KW somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMV;
 KW foot and mouth disease virus; immunoglobulin E; IGE; anti-allergic;
 KW Plasmodium falciparum; circumsporozoite; antimalarial; CEMP;
 KW cholesterol ester transport protein; anti-arteriosclerotic.

XX Homo sapiens.

OS Synthetic.

XX WO9966957-A2.

XX 29-DEC-1999.

XX 21-JUN-1999; 99WO-US13975.

XX 20-JUN-1998; 98US-0100412.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY;

XX WPI: 2000-160564/14.
 DR New artificial T helper cell epitope and derived immunogens with target
 XX antigenic site, for immunization against e.g. malaria, arteriosclerosis
 PT or human immune deficiency virus
 XX
 PS Example 6; Page 40; 129pp; English.

CC The invention relates to novel promiscuous T helper cell epitopes (Th),
 CC and immunogenic peptides comprising the Th epitopes of the invention
 CC along with B cell epitopes. The Th epitopes and peptide immunogens
 CC containing them, are used to induce a T helper cell response,
 CC specifically against Plasmodium falciparum, cholesteryl ester transport
 CC protein (CEP) or HIV epitopes, but more generally against any pathogen,
 CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
 CC peptide immunogens may be used for prevention and/or treatment of
 CC infections (HIV, foot-and-mouth disease or malaria); for cancer
 CC immunotherapy; for inhibition of the action of luteinising hormone
 CC releasing hormone (LHRH) for contraception, treatment of hormone-
 CC dependent cancer, prevention of boar taint in meat, and
 CC immunocastration); for promoting the growth of animals; or for
 CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
 CC Th (functional in genetically diverse subjects) into an immunogen
 CC improves capacity to induce a strong T helper cell-mediated immune
 CC response, resulting in production of antibodies against a target
 CC antigen. Th can replace carrier proteins and pathogen-derived T helper
 CC epitopes. Sequence AAY91121 represents a promiscuous T helper epitope
 CC from the measles virus F (WVF) protein and sequences AAY91122-Y91142,
 CC AAY91226 and AAY91245-Y91246 represent synthetic Th epitopes based on the
 CC MVR Th epitope. Sequence AAY91143 represents a promiscuous Th epitope
 CC from hepatitis B virus (HBV) surface antigen, and sequences
 CC AAY91144-Y91155 are synthetic epitopes derived from this HBV epitope.
 CC AAY91156-Y91196, AAY91227 and AAY91242-Y91244 are antigenic peptides
 CC comprising an LHRH sequence joined to a promiscuous Th epitope. AAY91197
 CC is the LHRH target antigenic peptide used in these LHRH antigenic
 CC peptides. AAY91200 is somatostatin, and AAY91201-Y91207 are antigenic
 CC peptides comprising somatostatin and a Th epitope. Somatostatin
 CC immunogens may be used to promote growth in livestock. AAY91208 is a
 CC human CD4 CDR2-like domain antigenic site, and AAY91209-Y92011 are MVR Th
 CC epitope/CD4 CDR2 antigenic peptides which may be used to prevent HIV
 CC infection of T cells. AAY90212 is a modified version of a human IGE
 CC (immunoglobulin E) CH3 domain, and AAY90213-Y90219 are Th epitope/IGE CH3
 CC antigenic peptides which may be used in the treatment of allergies
 CC AAY91220 is a peptide derived from foot and mouth disease virus (FMDV)
 CC VP1 capsid protein and AAY91221-Y91222 comprise this peptide and a Th
 CC epitope. AAY91223 is a Plasmodium falciparum circumsporozoite (CS) target
 CC antigen, and AAY91224-Y91225 comprise the CS antigen and an MVR Th
 CC epitope and may be used in a malaria vaccine. AAY91228-Y91231 represent
 CC CEP-derived peptides and AAY91232-Y91241 are immunogens comprising a
 CC CEP peptide and a Th epitope which may be used to prevent or treat
 CC arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-Y91257
 CC are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and
 CC AAY91258-Y91273 are antigenic peptides comprising MVR Th and HIV-1 B-cell
 CC epitope which may be used as a component in an anti-HIV-1 vaccine.
 CC AAY91198 and AAY91199 are respectively an immunostimulatory invasive
 CC protein epitope from *Yersinia* species, and hinge spacer peptide, both of
 CC which may optionally be used in the antigenic peptides of the
 CC invention.
 XX
 SQ Sequence 25 AA:

Query Match 47.1%; Score 64; DB 21; Length 25;
 Best Local Similarity 64.7%; Pred. No. 0.006;
 Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 RYTHPHLPKDIYRSIAK 18
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 Db 8 RYTHPHLPKDIYRSIAK 24

RESULT 12

AAY68602
 ID AAY68602 standard; peptide: 25 AA.
 XX
 AC AAY68602;
 XX
 DT 05-MAY-2000 (first entry)
 XX
 DE Peptide sequence of the invention.

KW Helper T cell epitope; peptide immunogen; LHRH;
 KW luteinising hormone-releasing hormone; spermatogenesis; ovulation;
 KW oestrus; sexual development; sex hormone; promiscuous T helper epitope;
 KW vaccine; contraceptive; hormone-dependent tumour; prostate cancer;
 KW breast cancer; endometriosis; boar taint; meat quality; immunocastration.

OS Unidentified.

PM W09966952-A1.

PD 29-DEC-1999.

PF 21-JUN-1999; 99WO-US13960.

PR 20-JUN-1998; 98US-0100414.

PA (UNBI-) UNITED BIOMEDICAL INC.

PI Wang CY;

DR WPI: 2000-160562/14.

PT New peptide immunogen containing luteinising hormone-releasing hormone
 PT antigen site and helper T cell epitope, for e.g. contraception and
 PT treatment of cancer
 PS Disclosure: Page 92; 102pp; English.

CC The specification describes peptide immunogens comprising a
 CC synthetic helper T cell (Th) epitope and a target antigen, luteinising
 CC hormone-releasing hormone (LHRH). The peptide immunogens cause
 CC induction of a specific immune response to LHRH which is involved in
 CC regulation of spermatogenesis, ovulation, oestrus, sexual development
 CC and secretion of sex hormones. Provision of a promiscuous T helper
 CC epitope (which is functional in genetically diverse subjects) provides
 CC optimum immunogenicity to the B cell epitopes of the target antigen and
 CC thus high antibody titres against the target antigen. The peptide
 CC immunogens of the invention are used to vaccinate against mammalian LHRH,
 CC for use as (reversible) contraceptive; control of hormone-dependent
 CC tumours (cancer of prostate or breast, also endometriosis); to prevent
 CC boar taint (and improve meat quality) and for immunocastration. The
 CC present sequence appears in the specification.

SQ Sequence 25 AA:

Query Match 47.1%; Score 64; DB 21; Length 25;
 Best Local Similarity 64.7%; Pred. No. 0.006;
 Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 RYTHPHLPKDIYRSIAK 18
 ||||| |
 Db 8 RYTHPHLPKDIYRSIAK 24

RESULT 13
 AAY80077
 ID AAY80077 standard; peptide: 25 AA.

AC AAY80077;

DT 15-MAY-2000 (first entry)

DE Optimised IGE-CH3 domain antigen peptide for horse IGE.

PT Immunoglobulin E variants as peptide antagonists useful for raising and
PT screening anti-immunoglobulin E (IGE) antibodies, in the isolation and
PT purification of FcepsilonRI receptor and in the treatment of allergic
PT diseases -

XX
XX
PS Disclosure; Column 9; 37pp; English.

CC The invention provides immunoglobulin E (IgE) antagonists comprising one
CC or more of the FcepsilonRI receptor-binding determinant sites of human
CC IGE. The antagonists include IGE variants comprising an immunoglobulin
CC template and binding determinant sequences (bds) CDDs, EFDs and the
CC sequence shown in AA42581. The CDDs (CD loop binding determinant
CC sequence) are selected from the sequences shown in AA42567-Y42577 and
CC the EFDs (EF loop binding determinant sequence) are selected from
CC sequences shown in AA42578-Y42580. The variants are useful in raising
CC and screening anti-IGE antibodies, in the isolation and purification of
CC FcepsilonRI receptor and in the treatment and prophylaxis of allergic
CC diseases.

XX
SQ Sequence 22 AA;

Query Match 44.1%; Score 60; DB 20; Length 22;

Best Local Similarity 69.2%; Pred. No. 0.021;

Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 CRVTHPHLPKDIV 13

Db 10 crvthphlprelm 22

Search completed: July 15, 2002, 12:50:18
Job time: 214 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 15, 2002, 12:47:04 ; Search time 12.87 Seconds
(without alignments)
47.447 Million cell updates/sec

Title: US-09-938-700-4

Sequence: 1 CRYTHPHLPKDIVRSIAKAPKRAP 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 134663

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep.*
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4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PCOTUS.COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/BACKFILE1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | ID | Description |
|------------|-------|--------------------|-------------------------|-------------------|
| 1 | 64 | 47.1 | 25 3 US-09-100-414B-95 | Sequence 95, Appl |
| 2 | 64 | 47.1 | 25 4 US-09-303-323-95 | Sequence 95, Appl |
| 3 | 60 | 44.1 | 22 2 US-08-232-539D-19 | Sequence 19, Appl |
| 4 | 60 | 44.1 | 24 2 US-08-232-539D-20 | Sequence 20, Appl |
| 5 | 36 | 26.5 | 18 2 US-09-017-205-52 | Sequence 52, Appl |
| 6 | 36 | 26.5 | 22 2 US-08-455-079-18 | Sequence 18, Appl |
| 7 | 36 | 26.5 | 23 2 US-08-455-079-14 | Sequence 12, Appl |
| 8 | 35.5 | 26.1 | 22 1 US-07-988-925-12 | Sequence 12, Appl |
| 9 | 35.5 | 26.1 | 22 2 US-08-362-780-12 | Sequence 4, Appl |
| 10 | 35 | 25.7 | 22 3 US-09-046-985-4 | Sequence 4, Appl |
| 11 | 35 | 25.7 | 22 4 US-09-474-743-4 | Sequence 4, Appl |
| 12 | 35 | 25.7 | 23 3 US-08-851-843A-208 | Sequence 208, App |
| 13 | 35 | 25.7 | 23 4 US-08-854-549A-327 | Sequence 327, App |
| 14 | 35 | 25.7 | 23 4 US-08-854-050-208 | Sequence 208, App |
| 15 | 35 | 25.7 | 23 4 US-09-430-323-208 | Sequence 15, Appl |
| 16 | 34 | 25.0 | 12 2 US-08-323-686-15 | Sequence 80, Appl |
| 17 | 34 | 25.0 | 21 2 US-08-480-190-80 | Sequence 80, Appl |
| 18 | 34 | 25.0 | 21 2 US-08-488-379-80 | Sequence 80, Appl |
| 19 | 34 | 25.0 | 21 5 PCR-US93-07545-80 | Sequence 80, Appl |
| 20 | 32 | 23.5 | 20 1 US-07-678-974D-17 | Sequence 17, Appl |
| 21 | 32 | 23.5 | 20 2 US-08-945-168-22 | Sequence 22, Appl |
| 22 | 32 | 23.5 | 24 4 US-08-818-253-15 | Sequence 15, Appl |
| 23 | 32 | 23.5 | 24 4 US-08-818-252-15 | Sequence 15, Appl |
| 24 | 31.5 | 23.2 | 15 2 US-08-934-222-87 | Sequence 87, Appl |
| 25 | 31.5 | 23.2 | 15 2 US-08-933-402-87 | Sequence 87, Appl |
| 26 | 31.5 | 23.2 | 15 2 US-09-207-621-87 | Sequence 87, Appl |
| 27 | 31.5 | 23.2 | 15 2 US-08-532-818-87 | Sequence 87, Appl |

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|----|------|------|-------------------------|-------------------|
| 28 | 31.5 | 23.2 | 15 3 US-09-231-797-87 | Sequence 87, Appl |
| 29 | 31.5 | 23.2 | 15 3 US-08-934-224-87 | Sequence 87, Appl |
| 30 | 31.5 | 23.2 | 15 3 US-08-933-843-87 | Sequence 87, Appl |
| 31 | 31.5 | 23.2 | 15 4 US-08-934-223-87 | Sequence 87, Appl |
| 32 | 31.5 | 23.2 | 15 4 US-09-413-492-87 | Sequence 87, Appl |
| 33 | 31 | 22.8 | 14 5 PCR-US93-06751-103 | Sequence 103, App |
| 34 | 31 | 22.8 | 15 2 US-08-455-079-5 | Sequence 5, Appl |
| 35 | 31 | 22.8 | 22 1 US-08-148-209A-9 | Sequence 9, Appl |
| 36 | 31 | 22.8 | 24 3 US-08-593-500-27 | Sequence 27, Appl |
| 37 | 31 | 22.8 | 24 3 US-08-195-006-27 | Sequence 27, Appl |
| 38 | 31 | 22.8 | 24 5 PCR-US94-07644A-27 | Sequence 891, App |
| 39 | 30 | 22.1 | 10 3 US-08-433-854-22 | Sequence 22, Appl |
| 40 | 30 | 22.1 | 12 1 US-08-174-745A-22 | Sequence 22, Appl |
| 41 | 30 | 22.1 | 12 1 US-08-195-947-22 | Sequence 22, Appl |
| 42 | 30 | 22.1 | 12 2 US-08-433-885-22 | Sequence 22, Appl |
| 43 | 30 | 22.1 | 12 2 US-08-433-908B-22 | Sequence 22, Appl |
| 44 | 30 | 22.1 | 12 2 US-08-410-614-22 | Sequence 22, Appl |
| 45 | 30 | 22.1 | 12 4 US-08-410-614-22 | Sequence 22, Appl |

ALIGNMENTS

RESULT 1
US-09-100-414B-95
; Sequence 95, Application US/09100414B
; Patent No. 6025468
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Y1
; TITLE OF INVENTION: NOVEL LRRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,414B
; FILING DATE: 20-JUNE-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-751-6849
; TELEFAX: 212-751-4800
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: Linear
; MOLECULE TYPE: peptide
; US-09-100-414B-95

Query Match 47.1%; Score 64; DB 3; Length 25;
Best Local Similarity 64.7%; Pred. No. 0.0012;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
OY 2 RYTHPHLPKDIVRSIAK 18
|||||||:|
DB 8 RYTHPHLPKALMRSTTK 24

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RESULT 2
US-09-303-323-95
; Sequence 95, Application US/09303323
; Patent No. 6228987
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Y1
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; TITLE OF INVENTION: IMMUNOGENS
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Flinnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/303,323
; FILING DATE: 30-Apr-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/100,414
; FILING DATE: 20-JUNE-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; US-09-303-323-95

Query Match 47.1% Score 64; DB 4; Length 25;
Best Local Similarity 64.7%; Pred. No. 0.0012;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Caps 0;

QY 2 RYTHPHLPKDIYRSIAK 18
DB 8 RYTHPHLPALMRSTTK 24

RESULT 3
US-08-232-539D-19
; Sequence 19, Application US/08232539D
; Patent No. 5965709
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: IGE Antagonists
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,539D
; FILING DATE: 21-Apr-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/178583
; FILING DATE: 07-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9861
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SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,539D
; FILING DATE: 21-Apr-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/178583
; FILING DATE: 07-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9861

US-08-232-539D-19

Query Match 44.1% Score 60; DB 2; Length 22;
Best Local Similarity 69.2%; Pred. No. 0.0045;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Caps 0;

QY 1 CRVTHPHLPKDIY 13
DB 10 CRVTHPHLPALM 22

RESULT 4
US-08-232-539D-20
; Sequence 20, Application US/08232539D
; Patent No. 5965709
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: IGE Antagonists
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,539D
; FILING DATE: 21-Apr-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/178583
; FILING DATE: 07-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9861
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; Sequence 4, Application US/09046985
; Patent No. 6121236
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel A.
; TITLE OF INVENTION: NOVEL MULTIVALENT LIGANDS WHICH MODULATE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millitia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,985
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: CMCC-614
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
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; OTHER INFORMATION: /note="N-Acetyl Alanine"
US-09-046-985-4

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Best Local Similarity 40.0%; Pred. No. 37;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 7 HRPKDIVRSIAKPG 21
| | | | : : | |
DB 8 HRPKDLXSVRRADG 22

RESULT 11
US-09-474-743-4
; Sequence 4, Application US/09474743
; Patent No. 6235716
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel A.
; TITLE OF INVENTION: NOVEL MULTIVALENT LIGANDS WHICH MODULATE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millitia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,985
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: CMCC-614
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /label="modified aa"
; OTHER INFORMATION: /note="N-Acetyl Alanine"
US-09-474-743-4

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/474,743
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/046,985
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: CMCC-614
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 861-6240
TELEFAX: (781) 861-9540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /label="modified aa"
OTHER INFORMATION: /note="N-Acetyl Alanine"
US-09-474-743-4

Query Match 25.7%; Score 35; DB 4; Length 22;
Best Local Similarity 40.0%; Pred. No. 37;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 7 HRPKDIVRSIAKPG 21
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DB 8 HRPKDLXSVRRADG 22

RESULT 12
US-08-851-843A-208
; Sequence 208, Application US/08851843A
; Patent No. 6093809
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin H.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6093809el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/851,843A
; FILING DATE: 06-MAY-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997

GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morlin, Gregg B.
APPLICANT: Hatley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017

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1 RESULT 14
2 US-08-854-050-208
3 Sequence 208, Application US/08854050
4 Patent No. 6261836
5
6 GENERAL INFORMATION:
7
8 APPLICANT: Cech, Thomas R.
9 APPLICANT: Lingner, Joachim
10 APPLICANT: Nakamura, Toru
11 APPLICANT: Chapman, Karen B.
12 APPLICANT: Morin, Gregg B.
13 APPLICANT: Hartley, Calvin
14 APPLICANT: Andrews, William H.
15 TITLE OF INVENTION: No. 6261836el Telomerase
16
17 NUMBER OF SEQUENCES: 225
18
19 CORRESPONDENCE ADDRESS:
20 ADDRESSEE: Townsend and Crew LLP
21 STREET: Two Embarcadero Center, 8th Floor
22 CITY: San Francisco
23 STATE: California
24 COUNTRY: United States of America
25 ZIP: 94111
26
27 COMPUTER READABLE FORM:
28 MEDIUM TYPE: Floppy disk
29
30 COMPUTER: IBM PC compatible
31 OPERATING SYSTEM: PC-DOS/MS-DOS

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1      SOFTWARE: PatentIn Release #1.0, Version #1.30
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3      CURRENT APPLICATION DATA:
4      APPLICATION NUMBER: US/08/854,050
5      FILING DATE: 09-MAY-1997
6      CLASSIFICATION: 536
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8      PRIOR APPLICATION DATA:
9      APPLICATION NUMBER: US 08/851,843
10     FILING DATE: 06-MAY-1997
11     CLASSIFICATION: 536
12
13     PRIOR APPLICATION DATA:
14     APPLICATION NUMBER: US 08/846,017
15     FILING DATE: 25-APR-1997
16     CLASSIFICATION: 536
17
18     PRIOR APPLICATION DATA:
19     APPLICATION NUMBER: US 08/844,419
20     FILING DATE: 18-APR-1997
21     CLASSIFICATION: 536
22
23     PRIOR APPLICATION DATA:
24     APPLICATION NUMBER: US 08/724,643
25     FILING DATE: 01-OCT-1996
26     CLASSIFICATION: 536
27
28     ATTORNEY/AGENT INFORMATION:
29     NAME: Apple, Randolph T.
30     REGISTRATION NUMBER: 36,429
31     REFERENCE/DOCKET NUMBER: 015389-00293005
32
33     TELECOMMUNICATION INFORMATION:
34     TELEPHONE: (415) 576-0200
35     TELEFAX: (415) 576-0300
36
37     INFORMATION FOR SEQ ID NO: 20:
38     SEQUENCE CHARACTERISTICS:
39     LENGTH: 23 amino acids
40     TYPE: amino acid
41     STRANDEDNESS:
42     TOPOLOGY: linear
43
44     MOLECULE TYPE: peptide
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46     US-08-854-050-208

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| Best Local Similarity | 38.5%; | Pred. NO. 39; | | |
| Matches 10; | Conservative 1; | Mismatches 3; | Indels 12; | Gaps 2; |

RESULT 15
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 : Sequence 208 Application US/09430323
 : Patent No. 6309867
 : GENERAL INFORMATION:
 APPLICANT: Cecch, Thomas R.
 Laigner, Joachim
 Nakamura, Toru
 Chapman, Karen B.
 Morlin, Gregg B.
 Harley, Calvin
 Andrews, William H.
 TITLE OF INVENTION: No. 6309867el Telomerase
 NUMBER OF SEQUENCES: 225
 CORRESPONDENCE ADDRESS:
 ADDRESS: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, 8th Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: United States of America
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

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1 CURRENT APPLICATION DATA:
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3 FILING DATE: 29-Oct-1999
4 CLASSIFICATION: <Unknown>
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6 PRIOR APPLICATION DATA:
7 APPLICATION NUMBER: US 08/854,050
8 FILING DATE: 09-MAY-1997
9 APPLICATION NUMBER: US 08/851,843
10 FILING DATE: 06-MAY-1997
11 APPLICATION NUMBER: US 08/846,017
12 FILING DATE: 25-APR-1997
13 APPLICATION NUMBER: US 08/844,419
14 FILING DATE: 18-APR-1997
15 APPLICATION NUMBER: US 08/724,643
16 FILING DATE: 01-OCT-1996
17
18 ATTORNEY/AGENT INFORMATION:
19 NAME: Apple, Randolph T
20 REGISTRATION NUMBER: 36,429
21 REFERENCE/DOCKET NUMBER: 015389-002930US
22 TELECOMMUNICATION INFORMATION:
23 TELEPHONE: (415) 576-0200
24 TELEFAX: (415) 576-0300
25
26 INFORMATION FOR SEQ ID NO: 208:
27
28 SEQUENCE CHARACTERISTICS:
29
30 LENGTH: 23 amino acids
31 TYPE: amino acid
32 STRANDEDNESS: <unknown>
33 TOPOLOGY: linear
34 MOLECULE TYPE: peptide
35 SEQUENCE DESCRIPTION: SEQ ID NO: 208:
36
37 US-09-430-323-208

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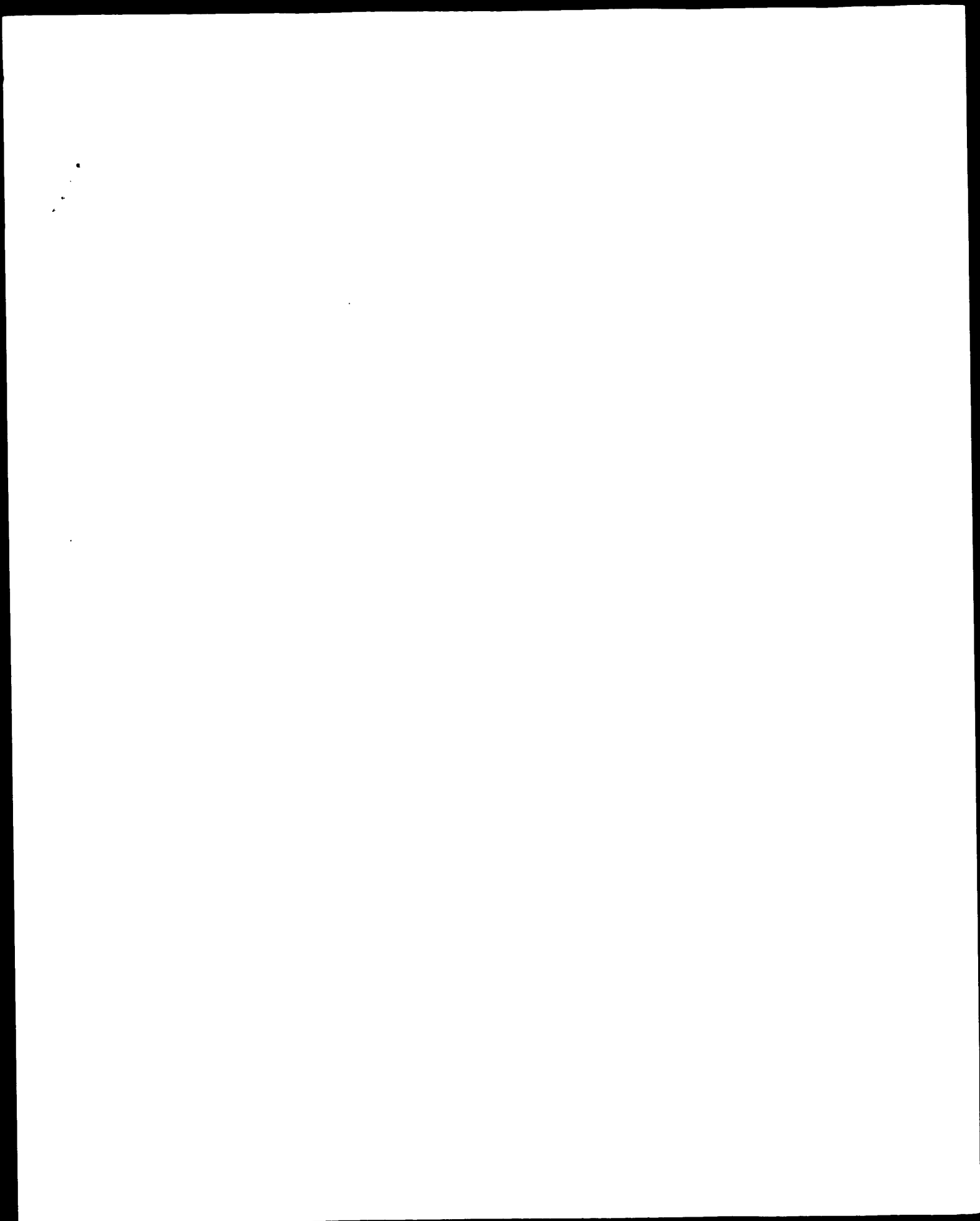
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Matches 10; Conservative 1; Mismatches 3; Indels 12; Gaps 2.

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          |||      |||
Db       6 TSPHRENLPD-----PGRCP 23

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Job time: 214 sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 15, 2002, 12:48:59 ; Search time 14.14 Seconds
(without alignments)
169,889 Million cell updates/sec

Title: US-09-938-700-4

Sequence: 1 CRVTHPLPKDVRSIKAPGKRAP 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 4981

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length DB | ID | Description |
|------------|-------|---------------|-----------|----|----------------------|
| 1 | 29 | 21.3 | 25 | 2 | histone H2B.1, spe |
| 2 | 28 | 20.6 | 11 | 2 | ribosomal protein |
| 3 | 27 | 19.9 | 16 | 2 | ig heavy chain DJ |
| 4 | 27 | 19.9 | 20 | 2 | acid ribonuclease |
| 5 | 27 | 19.9 | 25 | 1 | gene J protein - P |
| 6 | 26.5 | 19.5 | 20 | 2 | granulocyte inhibi |
| 7 | 26.5 | 19.5 | 22 | 2 | polygalacturonase |
| 8 | 26 | 19.1 | 13 | 2 | glutathione transf |
| 9 | 26 | 19.1 | 15 | 4 | hypothetical TEL/M |
| 10 | 26 | 19.1 | 20 | 2 | ribosomal protein |
| 11 | 26 | 19.1 | 22 | 2 | ig kappa chain V-I |
| 12 | 26 | 19.1 | 22 | 2 | ig kappa chain V-I |
| 13 | 26 | 19.1 | 24 | 2 | ribosomal protein |
| 14 | 26 | 19.1 | 24 | 2 | bradykinin-potenti |
| 15 | 25 | 18.4 | 10 | 2 | superoxide dismuta |
| 16 | 25 | 18.4 | 15 | 2 | agrin - electric r |
| 17 | 25 | 18.4 | 15 | 2 | homobolitin IV - Am |
| 18 | 25 | 18.4 | 17 | 2 | flagellar motor - sw |
| 19 | 25 | 18.4 | 20 | 2 | ribosomal protein |
| 20 | 25 | 18.4 | 21 | 2 | glutamate-ammonia |
| 21 | 25 | 18.4 | 21 | 2 | kinetoplast DNA-as |
| 22 | 25 | 18.4 | 22 | 2 | hypothetical prote |
| 23 | 25 | 18.4 | 24 | 2 | somatotropin - At1 |
| 24 | 25 | 18.4 | 25 | 2 | bradykinin-potenti |
| 25 | 24 | 17.6 | 10 | 2 | outer layer protei |
| 26 | 24 | 17.6 | 20 | 2 | retinoid-X-recepto |
| 27 | 24 | 17.6 | 20 | 2 | ribosomal protein |
| 28 | 24 | 17.6 | 21 | 2 | hypothetical prote |
| 29 | 24 | 17.6 | 22 | 2 | hypothetical prote |

| | | | | | |
|----|------|------|----|---|--------------------|
| 30 | 24 | 17.6 | 22 | 2 | cytochrome-b5 redu |
| 31 | 23.5 | 17.3 | 23 | 2 | hypothetical prote |
| 32 | 23.5 | 17.3 | 23 | 2 | kinase-related tra |
| 33 | 23 | 16.9 | 10 | 2 | cytochrome-c oxida |
| 34 | 23 | 16.9 | 15 | 2 | hypothetical 1.5K |
| 35 | 23 | 16.9 | 16 | 2 | major allergen Myr |
| 36 | 23 | 16.9 | 16 | 2 | ig heavy chain DJ |
| 37 | 23 | 16.9 | 18 | 2 | histone H2B - mous |
| 38 | 23 | 16.9 | 19 | 2 | superoxide dismuta |
| 39 | 23 | 16.9 | 20 | 2 | Ca2+/calmodulin-de |
| 40 | 23 | 16.9 | 20 | 2 | T cell receptor V- |
| 41 | 23 | 16.9 | 21 | 2 | ATPase A1 subunit |
| 42 | 23 | 16.9 | 22 | 2 | stromelysin /BC 3. |
| 43 | 23 | 16.9 | 23 | 2 | probable act-2 reg |
| 44 | 23 | 16.9 | 23 | 2 | platelet aggregati |
| 45 | 22 | 16.2 | 7 | 2 | A44428 |

ALIGNMENTS

RESULT 1
S07770 histone H2B.1, sperm - sea urchin (Echinus esculentus) (fragment)
C:Species: Echinus esculentus
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 23-Feb-1997
C:Accession: S07770
R: Hill, C.S.; Thomas, J.O.
Eur. J. Biochem. 187, 145-153, 1990
A:Title: Core histone-DNA interactions in sea urchin sperm chromatin. The N-terminal
A:Reference number: S07769; MUID:90126812
A:Accession: S07770
A:Molecule type: protein
A:Residues: 1-25 <HIL>
C:Superfamily: histone H2B
C:Keywords: chromosomal protein; DNA binding; nucleosome core; nucleus

Query Match 21.3%, Score 29; DB 2; Length 25;
Best Local Similarity 62.5%; Pred. No. 1.3e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 18 KAPGKRAP 25
DB 4 KSPTRKSP 11

RESULT 2
S78765 ribosomal protein MRP-S24, mitochondrial - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: S78765
R: Graack, H.R.
submitted to the Protein Sequence Database, July 1999
A:Reference number: S78760
A:Accession: S78765
A:Molecule type: protein
A:Residues: 1-11 <GRA>
C:Keywords: mitochondrial
F:1-11/Product: ribosomal protein MRP-S24 (fragment) #status experimental <MAT>

Query Match 20.6%; Score 28; DB 2; Length 11;
Best Local Similarity 40.0%; Pred. No. 7.7e+02;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 HPHLPKDIYR 14
DB 2 HVDVPRDLTK 11

RESULT 3

PH1351
 19 heavy chain DJ region (clone C100-109B) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C:Accession: PH1351
 R:Masserman, R.; Gallil, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
 J. Exp. Med. 176, 1577-1581, 1992
 A:Title: Predominance of fetal type DJH joining in young children with B precursor lymph
 A:Reference number: PH1302; MUID:93094761
 A:Accession: PH1351
 A:Molecule type: DNA
 A:Residues: 1-16 <MAS>
 C:Keywords: heterotetramer; Immunoglobulin

Query Match 19.9%; Score 27; DB 2; Length 16;
 Best Local Similarity 50.0%; Pred. No. 1.6e+03;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 16 TAKAPGRAP 25
 DB 7 IGSTPGAREP 16

RESULT 4
 A4139
 acid ribonuclease (EC 3.1.-.-) - bovine (fragment)
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 21-Mar-1996
 C:Accession: A4139
 R:Ohgi, K.; Sanda, A.; Takizawa, Y.; Irie, M.
 J. Biochem. 103, 267-273, 1988
 A:Title: Purification of acid ribonucleases from bovine spleen.
 A:Reference number: A4139; MUID:88227899
 A:Accession: A4139
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-20 <OHG>
 C:Keywords: hydrolase

Query Match 19.9%; Score 27; DB 2; Length 20;
 Best Local Similarity 50.0%; Pred. No. 2e+03;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 5 HPHRKDI 12
 DB 9 HLYFPKDL 16

RESULT 5
 ZJBPG4
 gene J protein - phage G4
 C:Species: phage G4
 C:Date: 30-Nov-1979 #sequence_revision 30-Nov-1979 #text_change 28-Jul-2000
 C:Accession: A04259
 R:Goodson, G.N.; Barrell, B.G.; Staden, R.; Fiddes, J.C.
 Nature 276, 236-247, 1978
 A:Title: Nucleotide sequence of bacteriophage G4 DNA.
 A:Reference number: A93200; MUID:79053264
 A:Accession: A04259
 A:Molecule type: DNA
 A:Residues: 1-25 <GOD>
 A:Cross-references: GB:J02454; GB:M10724; GB:M11404; GB:V00657; NID:q15831; PIDN:CA2401
 C:Comment: Gene J protein is one of the structural components of the bacteriophage coat.
 C:Superfamily: phage phi-X174 gene J protein
 C:Keywords: DNA binding

Query Match 19.9%; Score 27; DB 1; Length 25;
 Best Local Similarity 43.8%; Pred. No. 2.5e+03;
 Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 8 LPKDIVSIKAPGR 23
 DB 1 MKKSIRSGKSKGAR 16

RESULT 6
 A36016
 granulocyte inhibitory protein - human
 C:Species: Homo sapiens (man)
 C:Date: 11-Jan-1991 #sequence_revision 11-Jan-1991 #text_change 30-May-1997
 C:Accession: A36016
 R:Hoerl, W.H.; Haag-Weber, M.; Georgopoulos, A.; Block, L.H.
 Proc. Natl. Acad. Sci. U.S.A. 87, 6353-6357, 1990
 A:Title: Physicochemical characterization of a polypeptide present in uremic serum th
 A:Reference number: A36016; MUID:90349614
 A:Accession: A36016
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-20 <HOE>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 19.5%; Score 26.5; DB 2; Length 20;
 Best Local Similarity 36.8%; Pred. No. 2.3e+03;
 Matches 7; Conservative 5; Mismatches 2; Indels 5; Gaps 1;
 QY 11 DIVR-----SIKAPGR 24
 DB 1 DIVWTSPTGLSPGGERA 19

RESULT 7
 P00143
 polygalacturonase (EC 3.2.1.15) p26 - evening primrose (fragment)
 C:Species: Oenothera orgensis (evening primrose)
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 06-Dec-1996
 C:Accession: P00143
 R:Brown, S.M.; Crouch, M.L.
 Plant Cell 2, 263-274, 1990
 A:Title: Characterization of a gene family abundantly expressed in Oenothera orgensis
 A:Reference number: J00992; MUID:93005658
 A:Accession: P00143
 A:Molecule type: mRNA
 A:Residues: 1-22 <BRO>
 A:Experimental source: pollen
 C:Comment: This protein is specifically translated in the pollens.
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 19.5%; Score 26.5; DB 2; Length 22;
 Best Local Similarity 38.1%; Pred. No. 2.6e+03;
 Matches 8; Conservative 3; Mismatches 9; Indels 1; Gaps 1;
 QY 1 CRVTHPLKDIVSIKAPGR 21
 DB 1 CTTNMQ-LFDITKYGAKGDG 20

RESULT 8
 S32551
 glutathione transferase (EC 2.5.1.18) mu (isoform pi 6.4) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Dec-1993 #sequence_revision 01-Dec-1995 #text_change 05-Jan-1996
 C:Accession: S32551; S32550
 R:Singhal, S.S.; Saxena, M.; Ahmad, H.; Awasthi, Y.C.
 Blochim. Biophys. Acta 1116, 137-146, 1992
 A:Title: Glutathione S-transferases of mouse liver: sex-related differences in the ex
 A:Reference number: S32548; MUID:92256466
 A:Accession: S32551
 A:Molecule type: protein
 A:Residues: 1-13 <SINI>

A:Experimental source: female
 A:Accession: S32550
 A:Molecule type: protein
 A:Residues: 1-13 <SIN>
 A:Experimental source: male
 C:Keywords: transferase

Query Match 19.1%; Score 26; DB 2; Length 13;
 Best Local Similarity 80.0%; Pred. No. 1.8e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RYRHP 6
 DB 9 RLTHP 13

RESULT 9
 138336
 hypothetical TEL/MNI mutant fusion protein type I - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 20-Apr-2000
 C:Accession: 138336
 R:Bu13, A.; Sherr, S.; van Baal, S.; van Bezouw, S.; van der Plas, D.; Van Kessel, A.G.
 Oncogene 10, 1511-1519, 1995
 A>Title: Translocation (12;22) (P13;q11) in myeloproliferative disorders results in fusi
 A:Reference number: 138031; MUID:95249265
 A:Accession: 138336
 A>Status: translated from GB/EMBL/DBD
 A:Molecule type: mRNA
 A:Residues: 1-15 <BUT>
 A:Cross-references: EMBL:X85026; NID:9971473; PIDN:CA59399.1; PID:9971474
 C:Comment: This sequence is the chimeric product of a translocation mutation.
 C:Genetics:
 A:Gene: ETV6/MNI; TEL/MNI
 A:Map position: 22q11/12p13
 C:Keywords: fusion protein

Query Match 19.1%; Score 26; DB 4; Length 15;
 Best Local Similarity 66.7%; Pred. No. 2.1e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 HLPNDI 12
 DB 6 HLPNDL 11

RESULT 10
 JP0055
 ribosomal protein L30 - Bacillus polymyxa (fragment)
 C:Species: Bacillus polymyxa
 C>Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 02-Sep-2000
 C:Accession: JP0055
 R:Ochi, K.
 submitted to JRPD, February 1994
 A:Description: Phylogenetic diversity in the genus Bacillus and comparative ribosomal pr
 A:Reference number: JF0042
 A:Accession: JP0055
 A:Molecule type: protein
 A:Residues: 1-20 <OCH>
 C:Superfamily: Escherichia coli ribosomal protein L30
 C:Keywords: protein biosynthesis; ribosome

Query Match 19.1%; Score 26; DB 2; Length 20;
 Best Local Similarity 50.0%; Pred. No. 2.7e+03;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 12 IVNSIAKAPG 21
 DB 7 LVRSIGRPG 16

RESULT 11
 H30608
 Ig kappa chain V-III region (Ste) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 30-May-1997
 C:Accession: H30608
 R:Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; S
 J. Immunol. 142, 3158-3163, 1989
 A>Title: Structural and idiotypic characterization of the L chains of human Igm autoa
 A:Reference number: A30601; MUID:89215279
 A:Accession: H30608
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-22 <GON>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 19.1%; Score 26; DB 2; Length 22;
 Best Local Similarity 40.0%; Pred. No. 3e+03;
 Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 15 SIAPKPKRA 24
 DB 10 TLSPSPGERA 19

RESULT 12
 D30609
 Ig kappa chain V-III regions (Jon and Mlt) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 30-May-1997
 C:Accession: D30609
 R:Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; S
 J. Immunol. 142, 3158-3163, 1989
 A>Title: Structural and idiotypic characterization of the L chains of human Igm autoa
 A:Reference number: A30601; MUID:89215279
 A:Accession: D30609
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-22 <GON>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 19.1%; Score 26; DB 2; Length 22;
 Best Local Similarity 40.0%; Pred. No. 3e+03;
 Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 15 SIAPKPKRA 24
 DB 10 TLSPSPGERA 19

RESULT 13
 B30609
 Ig kappa chain V-III region (She) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 30-May-1997
 C:Accession: B30609
 R:Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; S
 J. Immunol. 142, 3158-3163, 1989
 A>Title: Structural and idiotypic characterization of the L chains of human Igm autoa
 A:Reference number: A30601; MUID:89215279
 A:Accession: B30609
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-24 <GON>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

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 Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 15 SIKAPGRK 24
 : : : : :
 DB 10 TLSPSPERA 19

RESULT 14

JP0052
 ribosomal protein L30 - *Bacillus macquarlenensis* (fragment)

C:Species: *Bacillus macquarlenensis*

C:Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 02-Sep-2000

C:Accession: JP0052

R:Ochl, K.
 submitted to JIPID, February 1994

A:Description: Phylogenetic diversity in the genus *Bacillus* and comparative ribosomal pr

A:Reference number: JP0042

A:Accession: JP0052

A:Molecule type: protein

A:Residues: 1-24 <OCH>

C:Superfamily: *Escherichia coli* ribosomal protein L30

C:Keywords: protein biosynthesis; ribosome

Query Match 19.1%; Score 26; DB 2; Length 24;
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 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 12 IVRSIAKPG 21
 : : : : :
 DB 8 LVRSIGRPG 17

RESULT 15

H37196
 bradykinin-potentiating peptide 8 - *Island jararaca*

C:Species: *Bothrops insularis* (*Island jararaca*)

C:Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 05-Aug-1994

C:Accession: H37196

R:Cintrá, A.C.O.; Vieira, C.A.; Giglio, J.R.

J. Protein Chem. 9, 221-227, 1990

A:Title: Primary structure and biological activity of bradykinin potentiating peptides

A:Reference number: A37196; MUID:90351557

A:Accession: H37196

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-10 <CIN>

C:Keywords: pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 18.4%; Score 25; DB 2; Length 10;
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 DB 5 HPNIP 9

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OM protein - protein search, using sw model

Run on: July 15, 2002, 12:50:44 ; Search time 10.22 Seconds
(without alignments)
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Title: US-09-938-700-4

Perfect score: 136

Sequence: 1 CRVTHPLPKDIVRSIAKAPGKRAP 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 1503

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1 | 31 | 22.8 | 18 | 1 | CT1C_LITCI |
| 2 | 29 | 21.3 | 18 | 1 | CT1A_LITCI |
| 3 | 29 | 21.3 | 18 | 1 | H2B1_ECHES |
| 4 | 27 | 19.9 | 12 | 1 | PEK4_PERAM |
| 5 | 27 | 19.9 | 24 | 1 | DMS6_PHYBI |
| 6 | 27 | 19.9 | 25 | 1 | VGT_BP64 |
| 7 | 26.5 | 19.5 | 19 | 1 | TRP3_LEUMA |
| 8 | 26 | 19.1 | 13 | 1 | UP71_LITEN |
| 9 | 26 | 19.1 | 15 | 1 | UC06_MAIZE |
| 10 | 26 | 19.1 | 16 | 1 | CT12_LITCI |
| 11 | 26 | 19.1 | 18 | 1 | CT1D_LITCI |
| 12 | 25 | 18.4 | 10 | 1 | BPP8_BOTIN |
| 13 | 25 | 18.4 | 13 | 1 | AV11_LITRA |
| 14 | 25 | 18.4 | 13 | 1 | AV12_LITRA |
| 15 | 25 | 18.4 | 15 | 1 | MC42_RHOOP |
| 16 | 25 | 18.4 | 16 | 1 | CT13_LITCI |
| 17 | 25 | 18.4 | 17 | 1 | BOLA_MEGEP |
| 18 | 25 | 18.4 | 19 | 1 | TRP4_KLEAE |
| 19 | 25 | 18.4 | 20 | 1 | RC11_HALMA |
| 20 | 25 | 18.4 | 25 | 1 | CR23_LITCE |
| 21 | 25 | 18.4 | 25 | 1 | CR24_LITCE |
| 22 | 24 | 17.6 | 10 | 1 | BPP2_BOTIN |
| 23 | 24 | 17.6 | 15 | 1 | MAOX_CHICK |
| 24 | 24 | 17.6 | 16 | 1 | AV22_LITAU |
| 25 | 24 | 17.6 | 16 | 1 | AV23_LITAU |
| 26 | 24 | 17.6 | 16 | 1 | CT11_LITCI |
| 27 | 24 | 17.6 | 16 | 1 | HS_COTIA |
| 28 | 24 | 17.6 | 17 | 1 | AV31_LITRA |
| 29 | 24 | 17.6 | 17 | 1 | AV32_LITRA |
| 30 | 24 | 17.6 | 17 | 1 | AV33_LITRA |
| 31 | 24 | 17.6 | 18 | 1 | CT1B_LITCI |
| 32 | 24 | 17.6 | 20 | 1 | VMO2_CHICK |
| 33 | 24 | 17.6 | 23 | 1 | NIFD_ANASL |

| | | | | | |
|----|----|------|----|---|-------------|
| 34 | 23 | 16.9 | 10 | 1 | COXO_THIOB |
| 35 | 23 | 16.9 | 16 | 1 | AV21_LITRA |
| 36 | 23 | 16.9 | 16 | 1 | AV25_LITRA |
| 37 | 23 | 16.9 | 17 | 1 | RS13_PARDE |
| 38 | 23 | 16.9 | 18 | 1 | LVC_ESTAC |
| 39 | 23 | 16.9 | 20 | 1 | MIL7_BOVIN |
| 40 | 23 | 16.9 | 20 | 1 | SODM_HORVU |
| 41 | 23 | 16.9 | 21 | 1 | CPFA_TREPH |
| 42 | 23 | 16.9 | 23 | 1 | SODM_RANCA |
| 43 | 22 | 16.2 | 10 | 1 | GOM2_CHPER |
| 44 | 22 | 16.2 | 15 | 1 | DOMM_PSECA |
| 45 | 22 | 16.2 | 16 | 1 | MMPX_SOLITU |

ALIGNMENTS

RESULT 1
ID CT1C_LITCI STANDARD: PRT: 18 AA.
AC P81844;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE Citropin 1.2.4.
OS Litorea citropa (Australian blue mountains tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Litorea.
OX NCBI_TaxID=94770;
RN [1]
RP TISSUE=Skin.
RC MEDLINE=99435977; PubMed=10504394;
RA Wegener K.L., Mahnitz P.A., Carver J.A., Bowie J.H., Chia B.C.S.,
RT Wallace J.C., Tyler M.J.;
RT "Host defence peptides from the skin glands of the Australian blue
mountains tree-frog Litorea citropa. Solution structure of the
antibacterial peptide citropin 1.1.";
RL Eur. J. Biochem. 265:627-637(1999).
CC -I- TISSUE SPECIFICITY: DORSAL AND SUBVENTRAL SKIN GLANDS.
SQ SEQUENCE 18 AA; 1814 MW; 500BF78D515ABD7 CRC64;

Query Match 22.8%; Score 31; DB 1; Length 18;
Best Local Similarity 33.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
QY 11 DIVERSIAKAPGKRAP 25
Db 4 DIKKVASVGLASP 18

RESULT 2
ID CT1A_LITCI STANDARD: PRT: 18 AA.
AC P81838;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE Citropin 1.1.3.
OS Litorea citropa (Australian blue mountains tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Litorea.
OX NCBI_TaxID=94770;
RN [1]
RP TISSUE=Skin.
RC MEDLINE=99435977; PubMed=10504394;
RA Wegener K.L., Mahnitz P.A., Carver J.A., Bowie J.H., Chia B.C.S.,
RT Wallace J.C., Tyler M.J.;
RT "Host defence peptides from the skin glands of the Australian blue

RT mountains-tree-frog *Litoria cilirostris*. Solution structure of the
 RT antibacterial peptide cilirostrin 1.1.*;
 RL Eur. J. Biochem. 265:627-637(1999).
 CC -1- TISSUE SPECIFICITY: DORSAL AND SUBVENTRAL SKIN GLANDS.
 SQ SEQUENCE 18 AA; 1814 MW; 500BF778D51F98D7 CRC64;

Query Match 21.3%; Score 29; DB 1; Length 18;
 Best Local Similarity 26.7%; Pred. No. 3.3e+02;
 Matches 4; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

OY 11 DIVRSIAKAPKRAP 25
 DB 4 DVIRKVASVIGLASP 18

RESULT 3
 H2BL_ECHES STANDARD: PRT; 25 AA.
 AC P13281;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Histone H2B.1, sperm (Fragment).
 OS Echinus esculentus (Sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinoidae; Euechinoidae; Echinacea; Echinoida; Echinidae; Echinus.
 OX NCBI_TaxID=7648;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90126812; PubMed=2298202;
 RA Hill C.S., Thomas J.O.;
 RT "Core histone-DNA interactions in sea urchin sperm chromatin. The N-
 terminal tail of H2B interacts with linker DNA.";
 RL Eur. J. Biochem. 187:145-153(1990).
 CC -1- SUBUNIT: THE NUCLEOSOME IS AN OCTAMER CONTAINING TWO MOLECULES OF
 H2A, H2B, H3, AND H4; WHICH WRAP APPROXIMATELY 146 BP OF DNA.
 CC -1- SUBCELLULAR LOCATION: Nucleolus.
 DR PIR: S07770; S07770.
 DR InterPro: IPR000558; Histone_H2B.
 DR PROSITE: PS00357; HISTONE_H2B; PARTIAL.
 KW Nucleolar protein; Chromosomal protein; Nucleosome core; DNA-binding;
 KW Multigene family.
 FT NON_TER 25
 SQ SEQUENCE 25 AA; 2693 MW; 9842DD3D73A3A9EC CRC64;

Query Match 21.3%; Score 29; DB 1; Length 25;
 Best Local Similarity 62.5%; Pred. No. 4.6e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 18 KAPGKRAP 25
 DB 4 KSPYKSP 11

RESULT 4
 PK4_PERAM STANDARD: PRT; 12 AA.
 AC P82619;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pyrokinin-4 (Pea-PK-4) (XXPRU-amide).
 OS Periplaneta americana (American cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 OC Blattodea; Blattella; Periplaneta.
 OX NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Retrocerebral complex;

RX MEDLINE=99212469; PubMed=10196736;
 RA Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;
 RT "Differential distribution of pyrokinin-isoforms in cerebral and
 abdominal neurohemal organs of the American cockroach.";
 RL Insect Biochem. Mol. Biol. 29:139-144(1999).

Query Match 19.9%; Score 27; DB 1; Length 12;
 Best Local Similarity 66.7%; Pred. No. 4.2e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 7 HLPKDI 12
 DB 2 HLPKDV 7

RESULT 5
 DMS6_PHYBI STANDARD: PRT; 24 AA.
 AC P81490;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Dermaseptin BVI (Dermaseptin B6).
 OS Phyllomedusa bicolor (Two-colored leaf frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
 OX NCBI_TaxID=8393;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin;
 RX MEDLINE=98278974; PubMed=9614066;
 RA Charpentier S., Amiche M., Wester J., Youille V., Le Caer J.-P.,
 RA Nicolas P., Delour A.;
 RT "Structure, synthesis, and molecular cloning of dermaseptins B, a
 family of skin peptide antibiotics.";
 RL J. Biol. Chem. 273:14690-14697(1998).
 CC -1- FUNCTION: POSSESSES A POTENT ANTIMICROBIAL ACTIVITY AGAINST
 CC GRAM-POSITIVE AND GRAM-NEGATIVE BACTERIA. PROBABLY ACTS BY
 CC DISTURBING MEMBRANE FUNCTIONS WITH ITS AMPHIPHILIC STRUCTURE.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE DERMASEPTIN FAMILY.
 CC Antibiotic; Multigene family; Amphibian skin; Amidation.
 FT MOD_RES 24
 SQ SEQUENCE 24 AA; 2665 MW; B5987D7F50E08F4F CRC64;

Query Match 19.9%; Score 27; DB 1; Length 24;
 Best Local Similarity 50.0%; Pred. No. 8.5e+02;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 10 KDIVRSIAKA 19
 DB 4 KDITKNAGKA 13

RESULT 6

VGJ_BPG4
ID VGJ_BPG4 STANDARD: PRT: 25 AA.
AC P03652;
RT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 01-OCT-1996 (Rel. 34, Last annotation update)
DE Small core protein (J protein).
GN J.
OS Bacteriophage G4.
OC Viruses; ssDNA viruses; Microviridae; Microvirus.
OX NCBI_TaxID=10843;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=79053264; PubMed=714153;
RA Godson G.N., Bartell B.G., Straden R., Fiddes J.C.;
RT "Nucleotide sequence of bacteriophage G4 DNA.";
RL Nature 276:236-247(1978).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RX MEDLINE=96217890; PubMed=8642594;
RA McKenna R., Bowman B.R., Ijag L.L., Rossmann M.G., Fane B.A.;
RT "Atomic structure of the degraded procapsid particle of the
RT bacteriophage G4: induced structural changes in the presence of
RT calcium ions and functional implications.";
RL J. Mol. Biol. 256:736-750(1996).
CC -1- FUNCTION: THE J PROTEIN IS ASSOCIATED WITH THE DNA AND IS SITUATED
CC IN AN INTERIOR CLEFT OF THE F PROTEIN.
CC -1- SUBUNIT: THE VIRION IS COMPOSED OF 60 COPIES EACH OF THE F, G, AND
CC J PROTEINS, AND 12 COPIES OF THE H PROTEIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: J02454; AAA3322.1; -;
DR EMBL: V00657; CAA24018.1; -;
DR PIR: A04259; ZJBP64.
DR PDB: 1GFP; 03-APR-96.
KW Coat protein; DNA-binding; 3D-structure.
SQ SEQUENCE 25 AA; 2815 MW; 87B7AB0FFDD033 CRC64;
Query Match 19.9%; Score 27; DB 1; Length 25;
Best Local Similarity 43.8%; Pred. No. 8.9e+02;
Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
QY 8 LPKDIVRSIAKAPGKR 23
DB 1 MKKSIRSGSKSGAR 16
RESULT 7
TRP3.LEUMA
ID TRP3.LEUMA STANDARD: PRT: 19 AA.
AC P81735;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Tachykinin-related peptide 3 (LemTRP 3).
OS Leucophaea maderae (Madelira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE.
RC TISSUE=Midgut;
RX MEDLINE=97053012; PubMed=8897641;
RA Muren J.E., Naessel D.R.;

RT "Isolation of five tachykinin-related peptides from the midgut of
RT the cockroach Leucophaea maderae: existence of N-terminally extended
RT isoforms.";
RL Regul. Pept. 65:185-196(1996).
CC -1- FUNCTION: MYOACTIVE PEPTIDE. INCREASES THE AMPLITUDE AND FREQUENCY
CC OF SPONTANEOUS CONTRACTIONS AND TONUS OF HINDGUT MUSCLE.
CC -1- TISSUE SPECIFICITY: MIDGUT.
CC -1- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 19
SQ SEQUENCE 19 AA; 1930 MW; 99B5471A011625E5 CRC64;
Query Match 19.5%; Score 26.5; DB 1; Length 19;
Best Local Similarity 66.7%; Pred. No. 8e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 1; Gaps 1;
QY 18 KAPG-KRAP 25
DB 4 RAPGSKRAP 12
RESULT 8
UP71.LITEM
ID UP71.LITEM STANDARD: PRT: 13 AA.
AC P82050;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Uperlin 7.1 (Contains: Uperlin 7.1.1).
OS Litoria ewingi (Brown tree frog) (Ewing's tree frog).
OC Amphibia; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Euryptila; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Litoria.
OX NCBI_TaxID=104896;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Steinborner S.T., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "An unusual combination of peptides from the skin glands of Ewing's
RT tree frog, Litoria ewingi. Sequence determination and antimicrobial
RT activity.";
RL Aust. J. Chem. 50:889-894(1997).
CC -1- FUNCTION: UPERLIN 7.1 SHOWS ANTIBACTERIAL ACTIVITY AGAINST L. LACTIS
CC AND S. UBERIS. UPERLIN 7.1.1 IS INACTIVE.
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -1- MASS SPECTROMETRY: MW=1427; METHOD=FAH; RANGE=1-13.
CC -1- MASS SPECTROMETRY: MW=1184; METHOD=FAH; RANGE=3-13.
KW Amphibian skin; Antibiotic; Amidation.
FT PEPTIDE 13
FT PEPTIDE 3 13
FT MOD_RES 13 13
SQ SEQUENCE 13 AA; 1429 MW; DE17C7204CCE322 CRC64;
Query Match 19.1%; Score 26; DB 1; Length 13;
Best Local Similarity 55.6%; Pred. No. 6.4e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 11 DIVRSIAKA 19
DB 4 DVAKHIAA 12
RESULT 9
UC06.MAIZE
ID UC06.MAIZE STANDARD: PRT: 15 AA.
AC P80612;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 1131)
(Fragment).
DE

OS Zea mays (Maize).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
 CC Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE.
 RC Tissue=coleoptile;
 RA Tournet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
 RA Perrolier J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 RT genome analysis program."
 RL Theor. Appl. Genet. 93:997-1005(1996).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 6.8, ITS MW IS: 71.0 KDa.
 DR Maize-2DPAGE: P80612; COLEOPTILE.
 DR MaizeDB: 123930.
 FT NON_TER 1 1
 FT 15 15
 SQ SEQUENCE 15 AA: 1390 MW: 700522830F23D61 CRC64;

Query Match 19.1%; Score 26; DB 1; Length 15;
 Best Local Similarity 55.6%; Pred. No. 7.4e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 17 AAPEKRAP 25
 DB 2 AAAPRRKP 10

RESULT 10
 ID CT12_LITCI STANDARD: PRT: 16 AA.
 AC P81840; P81841; P81842; P81843;
 DT 30-MAY-2000 (Rel. 39; Created)
 DT 30-MAY-2000 (Rel. 39; Last sequence update)
 DT 16-OCT-2001 (Rel. 40; Last annotation update)
 DE Citropin 1.2 [Contains: Citropin 1.2.1; Citropin 1.2.2; Citropin 1.2.3].
 OS Litoria citropa (Australian blue mountains tree frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
 CC Litoria
 OX NCBI_TaxID=94770;
 RN [1]
 RP SEQUENCE.
 RC Tissue=Skin;
 RA MEDLINE=99435977; PubMed=10504394;
 RA Wegener K.L., Wabnitz P.A., Carver J.A., Bowie J.H., Chia B.C.S.,
 RA Wallace J.C., Tyler M.J.;
 RT "Host defence peptides from the skin glands of the Australian blue
 RT mountains tree-frog Litoria citropa. Solution structure of the
 RT antibacterial peptide citropin 1.1.";
 RL Eur. J. Biochem. 265:627-637(1999).
 CC -1- FUNCTION: BACTERIOSTATIC ACTION FOR GRAM-POSITIVE BACTERIA.
 CC -1- TISSUE SPECIFICITY: DORSAL AND SUBMENTAL SKIN GLANDS.
 KW Antibiotic; Amidation.
 FT PEPTIDE 1 16 CITROPIN 1.2.
 FT 3 14 CITROPIN 1.2.1
 FT 4 14 CITROPIN 1.2.2
 FT 1 11 CITROPIN 1.2.3
 FT PEPTIDE 1 16
 FT MOD_RES 16 16 IDB78515ABD73DE9 CRC64;
 SQ SEQUENCE 16 AA: 1616 MW: 16878515ABD73DE9 CRC64;

Query Match 19.1%; Score 26; DB 1; Length 16;
 Best Local Similarity 36.4%; Pred. No. 7.9e+02;
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 11 DIVRSIAKAPG 21
 DB 4 DIRKVASVG 14

RESULT 11
 ID CT12_LITCI STANDARD: PRT: 18 AA.
 AC P81845;
 DT 30-MAY-2000 (Rel. 39; Created)
 DT 30-MAY-2000 (Rel. 39; Last sequence update)
 DT 30-MAY-2000 (Rel. 39; Last annotation update)
 DE Citropin 1.2.5.
 OS Litoria citropa (Australian blue mountains tree frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
 CC Litoria
 OX NCBI_TaxID=94770;
 RN [1]
 RP SEQUENCE.
 RC Tissue=Skin;
 RA MEDLINE=99435977; PubMed=10504394;
 RA Wegener K.L., Wabnitz P.A., Carver J.A., Bowie J.H., Chia B.C.S.,
 RA Wallace J.C., Tyler M.J.;
 RT "Host defence peptides from the skin glands of the Australian blue
 RT mountains tree-frog Litoria citropa. Solution structure of the
 RT antibacterial peptide citropin 1.1.";
 RL Eur. J. Biochem. 265:627-637(1999).
 CC -1- TISSUE SPECIFICITY: DORSAL AND SUBMENTAL SKIN GLANDS.
 CC -1- TISSUE SPECIFICITY: DORSAL AND SUBMENTAL SKIN GLANDS.
 SQ SEQUENCE 18 AA: 1845 MW: 51BBF78D515ABD7 CRC64;

Query Match 19.1%; Score 26; DB 1; Length 18;
 Best Local Similarity 36.4%; Pred. No. 8.9e+02;
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 11 DIVRSIAKAPG 21
 DB 4 DIRKVASVG 14

RESULT 12
 ID BPP8_BOTIN STANDARD: PRT: 10 AA.
 AC P30426;
 DT 01-APR-1993 (Rel. 25; Created)
 DT 01-FEB-1994 (Rel. 28; Last sequence update)
 DT 01-FEB-1994 (Rel. 28; Last annotation update)
 DE Bradykinin-potentiating peptide 55.1 (Angiotensin-converting
 DE enzyme inhibitor).
 OS Bothrops insularis (Island jararaca) (Oueimada jararaca).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
 CC Viperidae; Crotalinae; Bothrops.
 OX NCBI_TaxID=8723;
 RN [1]
 RP SEQUENCE.
 RC Tissue=Venom;
 RA MEDLINE=90351557; PubMed=2386615;
 RA Cintrà A.C.O., Vieira C.A., Giglio J.R.;
 RT "Primary structure and biological activity of bradykinin potentiating
 RT peptides from Bothrops insularis snake venom.";
 RL J. Protein Chem. 9:221-227(1990).
 CC -1- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE
 CC ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF
 CC BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
 CC IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
 DR PIR: H37196; H37196.
 KW Hypotensive agent; Venom.
 FT MOD_RES 1 1
 FT 1 1
 SQ SEQUENCE 10 AA: 1175 MW: 2FF83545761F6D8 CRC64;

Query Match 18.4%; Score 25; DB 1; Length 10;
 Best Local Similarity 60.0%; Pred. No. 6.9e+02;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 5 HPHP 9
|:|:|
Db 5 HPNP 9

RESULT 13

ID AUI1_LITRA STANDARD; PRT; 13 AA.
AC P82386;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DE Aurein 1.1.
OS Litoria raniformis (Southern bell frog).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Litoria.
OX NCBI_Taxid=116057;
RN [1]

SEQUENCE AND FUNCTION.

RP TISSUE-granular dorsal gland.
RC MEDLINE=2040845; PubMed=10951191;
RA Rozek T., Wegener K.L., Bowie J.H., Oliver I.N., Carver J.A.,
Wallace J.C., Tyler M.J.;
RT "The antibiotic and anticancer active aurein peptides from the
RT Australian bell frogs Litoria aurea and Litoria raniformis the
RT solution structure of aurein 1.2".
RL Eur. J. Biochem. 267:5330-5341(2000).
CC -I- FUNCTION: ANTIMICROBIAL ACTIVITY AGAINST B.CEREUS, L.LACTIS,
CC L.INNOCUA AND S.UBERIS. PROBABLY ACTS BY DISTURBING MEMBRANE
CC FUNCTIONS WITH ITS AMPHIPATHIC STRUCTURE.
CC -I- SUBCELLULAR LOCATION: SECRETED.
KW Antibiotic; Amidation.
FT MOD_RES 13
SQ SEQUENCE 13 AA; 1447 MW; 173CB99DFBC83330 CRC64;

Query Match 18.4%; Score 25; DB 1; Length 13;
Best Local Similarity 44.4%; Pred. No. 9e+02;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 11 DIVRSIKA 19
|:|:|:|:|
Db 4 DIKKIAES 12

RESULT 14

ID AUI2_LITRA STANDARD; PRT; 13 AA.
AC P82387;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Aurein 1.2.
OS Litoria raniformis (Southern bell frog).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Litoria.
OX NCBI_Taxid=116057;
RN [1]

SEQUENCE, FUNCTION, AND STRUCTURE BY NMR.

RC TISSUE-granular dorsal gland.
RC MEDLINE=2040845; PubMed=10951191;
RA Rozek T., Wegener K.L., Bowie J.H., Oliver I.N., Carver J.A.,
Wallace J.C., Tyler M.J.;
RT "The antibiotic and anticancer active aurein peptides from the
RT Australian bell frogs Litoria aurea and Litoria raniformis the
RT solution structure of aurein 1.2".
RL Eur. J. Biochem. 267:5330-5341(2000).
CC -I- FUNCTION: ANTIMICROBIAL ACTIVITY AGAINST B.CEREUS, L.LACTIS,
CC L.INNOCUA, M.LUTEUS, P.MULTOCIDA, S.AUREUS, S.EPIDERMIDIS AND
CC S.UBERIS. PROBABLY ACTS BY DISTURBING MEMBRANE FUNCTIONS WITH ITS

CC -I- AMPHIPATHIC STRUCTURE. SHOWS ANTICANCER ACTIVITY.
CC -I- SUBCELLULAR LOCATION: SECRETED.
KW Amidation; Antibiotic.
FT MOD_RES 13
SQ SEQUENCE 13 AA; 1481 MW; 1EACB99DFBC83330 CRC64;

Query Match 18.4%; Score 25; DB 1; Length 13;
Best Local Similarity 44.4%; Pred. No. 9e+02;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 11 DIVRSIKA 19
|:|:|:|:|
Db 4 DIKKIAES 12

RESULT 15

ID MCA2_RHOOP STANDARD; PRT; 15 AA.
AC P56870;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative maleylacetate reductase II (EC 1.3.1.32) (Fragment).
OS Rhodococcus opacus (Nocardia opaca).
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Nocardaceae; Rhodococcus.
OX NCBI_Taxid=37919;
RN [1]

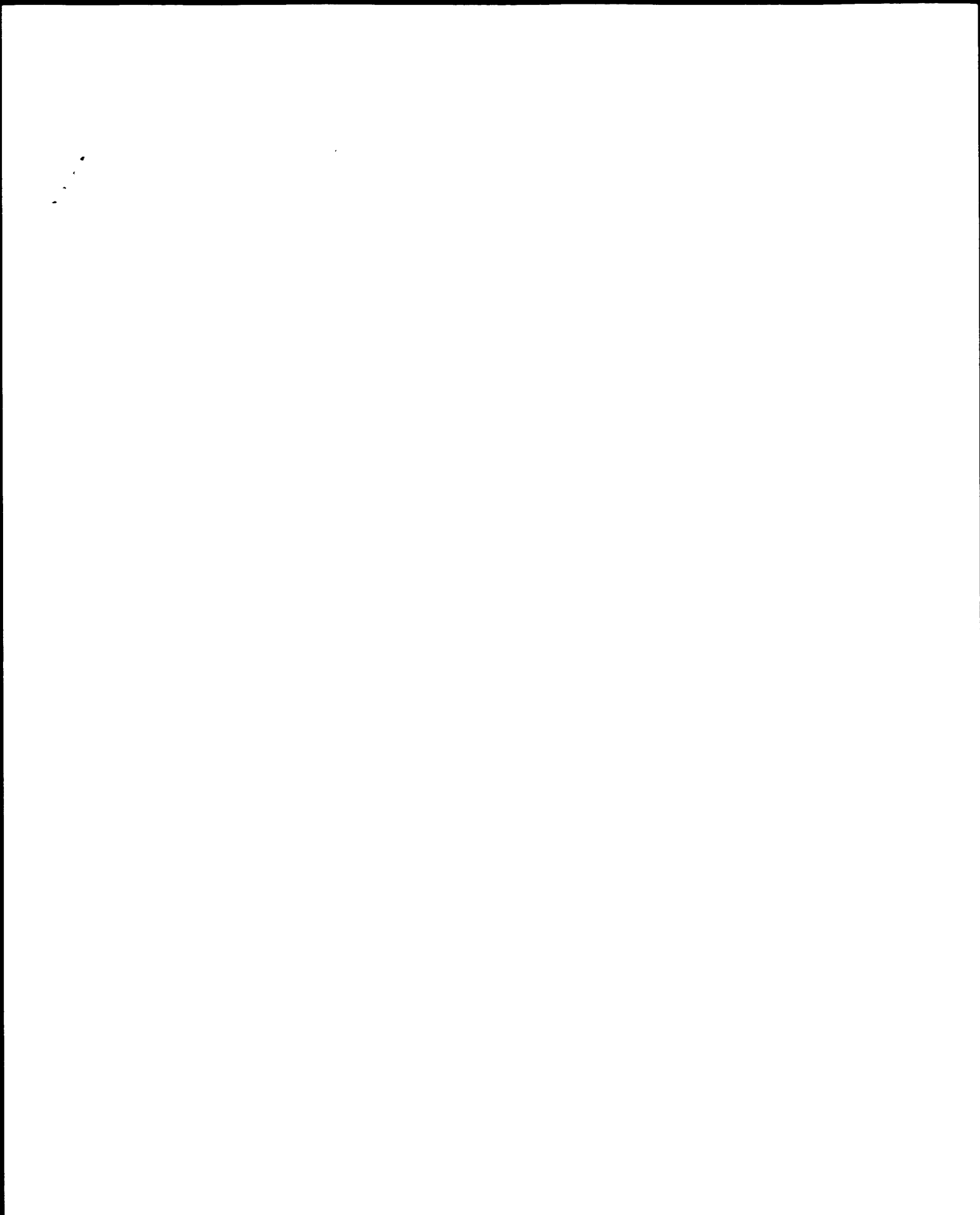
SEQUENCE.

RP STRAIN=ICP;
RC MEDLINE=98324954; PubMed=9657989;
RA Seibert V., Kourbatova E.M., Golovleva L.A., Schloemann M.;
RT "Characterization of a maleylacetate reductase encoding region from
RT Rhodococcus opacus ICP".
RL J. Bacteriol. 180:3503-3508(1998).
CC -I- CATALYTIC ACTIVITY: 3-oxoadipate + NAD(P)(+) = 2-maleylacetate +
CC NAD(P)H.
CC -I- PATHWAY: 3-CHLOROCATECHOL DEGRADATION (BETA-KETOADIPIRATE PATHWAY).
CC THIS PATHWAY SERVES A VITAL ROLE IN THE BIODEGRADATION OF TOXIC
CC AROMATIC COMPOUNDS INTRODUCED IN THE ENVIRONMENT BOTH AS NATURAL
CC PRODUCTS AND AS INDUSTRIAL EFFLUENT.
CC -I- SIMILARITY: BELONGS TO THE IRON-CONTAINING ALCOHOL DEHYDROGENASE
CC FAMILY.
DR InterPro: IPR001670; Fe-ADH.
DR PROSITE: PS00913; ADH_IRON_1; PARTIAL.
DR PROSITE: PS00060; ADH_IRON_2; PARTIAL.
KW Aromatic hydrocarbons catabolism; Oxidoreductase; NAD.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1884 MW; 58DA90DD008F025E CRC64;

Query Match 18.4%; Score 25; DB 1; Length 15;
Best Local Similarity 45.5%; Pred. No. 1e+03;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 2 RVTHPLPKDI 12
|:|:|:|:|
Db 2 RFEHENVLPQRI 12

Search completed: July 15, 2002, 12:53:59
Job time: 195 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 15, 2002, 12:50:24 ; Search time 23.8 seconds
(without alignments)
181.717 Million cell updates/sec

Title: US-09-938-700-4

Sequence: 1 CRVTHPLPKDIVRSINAKAPKRAP 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapect 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 8561

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP_TODENT:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*
15: SP_VIRILUS:*
16: SP_BACTERIAP:*
17: SP_ARCHAEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 30 | 22.1 | 18 | 4 | 09BOTO |
| 2 | 30 | 22.1 | 19 | 15 | 09ORH8 |
| 3 | 30 | 22.1 | 20 | 11 | 099IV2 |
| 4 | 29 | 21.3 | 16 | 8 | 09T2R0 |
| 5 | 29 | 21.3 | 19 | 4 | 016271 |
| 6 | 28 | 20.6 | 22 | 7 | 09MX47 |
| 7 | 28 | 20.6 | 24 | 2 | 09L7N8 |
| 8 | 27 | 19.9 | 15 | 4 | 09UEM3 |
| 9 | 27 | 19.9 | 20 | 4 | 09UM18 |
| 10 | 27 | 19.9 | 21 | 6 | 09N0J5 |
| 11 | 26.5 | 19.5 | 17 | 5 | 09TWR3 |
| 12 | 26.5 | 19.5 | 22 | 10 | 08S9B8 |
| 13 | 26 | 19.1 | 15 | 4 | 09UCJ8 |
| 14 | 26 | 19.1 | 16 | 8 | 09T2V8 |
| 15 | 26 | 19.1 | 18 | 6 | 095JA2 |
| 16 | 26 | 19.1 | 21 | 12 | 085667 |

| | | | | | | |
|----|------|------|----|----|--------|----------------------|
| 17 | 26 | 19.1 | 24 | 2 | 09L7N6 | 0917n6 borrellia bi |
| 18 | 26 | 18.1 | 25 | 11 | 09QW9 | 09quw9 rattus sp. |
| 19 | 25.5 | 18.8 | 16 | 6 | 09TRD1 | 09trd1 sus scrofa |
| 20 | 25.5 | 18.8 | 24 | 5 | 090542 | 09u542 aedes aegypti |
| 21 | 25 | 18.4 | 13 | 13 | P82386 | P82386 litorea ran |
| 22 | 25 | 18.4 | 13 | 13 | P82387 | P82387 litorea ran |
| 23 | 25 | 18.4 | 14 | 3 | P90342 | P90342 saccharomyces |
| 24 | 25 | 18.4 | 15 | 3 | 090403 | 090403 discopyge o |
| 25 | 25 | 18.4 | 17 | 6 | 09XSG1 | 09xsg1 bos taurus |
| 26 | 25 | 18.4 | 18 | 2 | 09R4R0 | 09r4r0 pseudomonas |
| 27 | 25 | 18.4 | 19 | 13 | 062416 | 062416 gallus gall |
| 28 | 25 | 18.4 | 19 | 15 | 09ORH4 | 09orh4 human immun |
| 29 | 25 | 18.4 | 21 | 4 | 09H428 | 09h428 homo sapien |
| 30 | 25 | 18.4 | 22 | 5 | 09TW08 | 09tw08 crithidia f |
| 31 | 25 | 18.4 | 22 | 13 | 09PS65 | 09ps65 oncorhynchus |
| 32 | 25 | 18.4 | 23 | 2 | 043887 | 043887 anabaena az |
| 33 | 25 | 18.4 | 23 | 5 | 09S595 | 09s595 drosophila |
| 34 | 25 | 18.4 | 23 | 10 | 094IS9 | 094is9 pinus taeda |
| 35 | 25 | 18.4 | 24 | 2 | 09KIT6 | 09kit6 streptomyces |
| 36 | 25 | 18.4 | 25 | 10 | 094IS2 | 094is2 pinus radia |
| 37 | 24.5 | 18.0 | 20 | 13 | 09PSH5 | 09psh5 gallus gall |
| 38 | 24 | 17.6 | 13 | 8 | 033417 | 033417 digitalis p |
| 39 | 24 | 17.6 | 15 | 11 | 09QV01 | 09qv01 mus sp. 16 |
| 40 | 24 | 17.6 | 16 | 5 | P82706 | P82706 drosophila |
| 41 | 24 | 17.6 | 16 | 13 | P82389 | P82389 litorea aur |
| 42 | 24 | 17.6 | 16 | 13 | P82390 | P82390 litorea aur |
| 43 | 24 | 17.6 | 17 | 2 | 034216 | 034216 sphingomona |
| 44 | 24 | 17.6 | 17 | 10 | 09SMC7 | 09smc7 lycopersicon |
| 45 | 24 | 17.6 | 17 | 13 | P82394 | P82394 litorea ran |

ALIGNMENTS

RESULT 1
ID 09BOTO PRELIMINARY: PRT: 18 AA.
AC 09BOTO
DT 01-JUN-2001 (TRMBLrel. 17, Created)
DT 01-JUN-2001 (TRMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TRMBLrel. 17, Last annotation update)
DE HYPOTHETICAL 2.2 KDA PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=21195339; PubMed=11297743;
RA Holzmann K., Ambrosch I., Eldling L., Micksche M., Berger W.;
RT "A small upstream open reading frame causes inhibition of human major
vault protein expression from a ubiquitous mRNA splice variant.";
RL FEBS Lett. 484:99-104(2001).
DR EMBL; AJ291367; CAC35315.1 -.
KW Hypothetical protein.
SQ SEQUENCE 18 AA; 2179 MW; 5D06F9A3F11C828 CRC64;

Query Match 22.1%; Score 30; DB 4; Length 18;
Best Local Similarity 66.7%; Pred. No. 9.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 1 CRVTHPLP 9
DB 8 CRL--PHLP 14
RESULT 2
ID 09ORH8 PRELIMINARY: PRT: 19 AA.
AC 09ORH8
DT 01-DEC-2001 (TRMBLrel. 19, Created)
DT 01-DEC-2001 (TRMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE TAT PROTEIN (FRAGMENT).
GN TAT.
OS Human Immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
RX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-96CG12;
RA Taniguchi Y., Takehisa J., Bikanou B., Mboudjeleka I.,
RA N'Doumou-N'Kodia M.-Y., Obengul, M'Pandi M., M'pele P., Harada Y.,
RA Hayami M., Ichimura H., Parra J.H.,
RT "Genetic Subtypes of HIV Type 1 Based on the vpr/env Sequences in
RT Republic of Congo-Brazzaville."
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF127545; AAK84896.1; .
FT NON_TER 1 19 1
FT NON_TER 19 19 1
SQ SEQUENCE 19 AA; 2210 MW; 2A83642B89068236 CRC64;

Query Match 22.1%; Score 30; DB 15; Length 19;
Best Local Similarity 53.8%; Pred. No. 1e+03;
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 6 PHLPKDIYRSIAK 18
DB 7 PHSKDHONSIPK 19

RESULT 3
O99JV2 PRELIMINARY; PRT; 20 AA.
AC O99JV2;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 2.2 KDA PROTEIN (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC005653; AAH05653.1; .
KW Hypothetical protein.
FT NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 20 AA; 2223 MW; F203F6A80A7A0429 CRC64;

Query Match 22.1%; Score 30; DB 11; Length 20;
Best Local Similarity 70.0%; Pred. No. 1.1e+03;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 13 VRSIAKAPK 22
DB 1 VESAKRPPK 10

RESULT 4
O972R0 PRELIMINARY; PRT; 16 AA.
AC O972R0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE CYTOCHROME-C REDUCTASE 14 KDA SUBUNIT (EC 1.10.2.2) (FRAGMENT).
OS Solanum tuberosum (Potato).
OG Mitochondrion.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots.

OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE.
RX MEDLINE=94198758; PubMed=7764624;
RA Braun H.P., Krut V., Schmitz U.K.,
RL Planta 193:99-106(1994).
SQ SEQUENCE 16 AA; 1946 MW; B6C625F8E4A4C8E7 CRC64;

Query Match 21.3%; Score 29; DB 8; Length 16;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 5 HPHLPKDI 12
DB 2 HOYLPEDL 9

RESULT 5
O16271 PRELIMINARY; PRT; 19 AA.
AC O16271;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ARGININE VASOPRESSIN V2 RECEPTOR (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=95086168; PubMed=7993996;
RA Holtzman E.J., Kolakowski L.F.Jr., Gelfman-Holtzman O., O'Brien D.G.,
RA Rasoulypour M., Guillot A.P., Ausiello D.A.;
RT "Mutations in the vasopressin V2 receptor gene in two families with
RT nephrogenic diabetes insipidus."
RL J Am Soc Nephrol 5:169-176(1994).
DR EMBL: S75754; AAB32753.1; .
KW Receptor.
FT NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 19 AA; 1905 MW; 181640EFD90F2788 CRC64;

Query Match 21.3%; Score 29; DB 4; Length 19;
Best Local Similarity 37.5%; Pred. No. 1.5e+03;
Matches 6; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

OY 5 HPHLPKDIYRSIAKAP 20
DB 4 HPSLPSCAWASLSAQF 19

RESULT 6
O9KX47 PRELIMINARY; PRT; 22 AA.
AC O9KX47;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MHC CLASS II ANTIGEN (FRAGMENT).
GN ORLA-DCB.
OS Oryzias latipes (Medaka fish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-HNI;
RA Naruse K., Oku H., Kojima A., Bessho Y., Kuroda N., Matsuzaki T.,

Best Local Similarity 46.7%; Pred. No. 3.2e+03;
Matches 7; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

OY 6 PHLPKDIYSIAKAP 20
DB 2 PILGKDPHKMAKAP 16

RESULT 11

O9TW83 PRELIMINARY; PRT: 17 AA.
AC O9TW83: 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE HISTONE H1 (FRAGMENT).
OS Trypanosoma cruzi.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5693;
RN [1]
RP SEQUENCE.
RX MEDLINE=94043510; PubMed=8227175;
RA Toro G.C., Galanti N., Hellman U., Wernstedt C.;
RT "Unambiguous identification of histone H1 in Trypanosoma cruzi."
RL J. Cell. Biochem. 52:431-439(1993).
SQ SEQUENCE 17 AA; 1820 MW; AD19BC52D8ECCD5 CRC64;

Query Match 19.5%; Score 26.5; DB 5; Length 17;
Best Local Similarity 40.0%; Pred. No. 3.1e+03;
Matches 6; Conservative 4; Mismatches 2; Indels 3; Gaps 1;

OY 9 PKDIVSIKAPKRR 23
DB 6 PK---KAVKAPKPKK 17

RESULT 12

O9S9B8 PRELIMINARY; PRT: 22 AA.
AC O9S9B8: 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE POLYGALACTURONASE HOMOLOG (FRAGMENT).
OS Oenothera organensis (Evening primrose).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Myrtales; Onagraceae; Oenothera.
OX NCBI_TaxID=3945;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93005658; PubMed=2152116;
RA Brown S.M., Crouch M.L.;
RT "Characterization of a gene family abundantly expressed in Oenothera
RT organensis pollen that shows sequence similarity to
RT polygalacturonase."
RL Plant Cell 2:263-274(1990).
SQ SEQUENCE 22 AA; 2289 MW; 2383FEFBA1E3C70 CRC64;

Query Match 19.5%; Score 26.5; DB 10; Length 22;
Best Local Similarity 38.1%; Pred. No. 4e+03;
Matches 8; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

OY 1 CRYTHPLPKDIYSIAKAPG 21
DB 1 CTTNAGL-FDITKYGAGDG 20

RESULT 13
O9UCJ8 PRELIMINARY; PRT: 15 AA.

AC O9UCJ8: 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE TYPE IV PROCOLLAGENASE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=93125366; PubMed=1480041;
RA Stetler-Stevenson W.G., Krutzsch H.C., Liotta L.A.;
RT "TIMP-2: identification and characterization of a new member of the
RT metalloproteinase inhibitor family."
RL Matrix Suppl. 1:299-306(1992).
SQ SEQUENCE 15 AA; 1537 MW; D5DA1MAA9C32276C CRC64;

Query Match 19.1%; Score 26; DB 4; Length 15;
Best Local Similarity 60.0%; Pred. No. 3.2e+03;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 16 IAKAPKRAP 25
DB 5 IIKFPGDAP 14

RESULT 14

O9T2V8 PRELIMINARY; PRT: 16 AA.
AC O9T2V8: 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE 2-ENOYL-COA HYDRATASE (FRAGMENT).
OS Homo sapiens (Human).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95046784; PubMed=7958339;
RA Middleton B.;
RT "The mitochondrial long-chain trifunctional enzyme: 2-enoyl-CoA
RT hydratase, 3-hydroxyacyl-CoA dehydrogenase and 3-oxoacyl-CoA
RT thiolase."
RL Biochem. Soc. Trans. 22:427-431(1994).
SQ SEQUENCE 16 AA; 1763 MW; 31AD66A3080B019A CRC64;

Query Match 19.1%; Score 26; DB 8; Length 16;
Best Local Similarity 31.2%; Pred. No. 3.4e+03;
Matches 5; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

OY 10 KDIVSIKAPKRAP 25
DB 1 KPNIRNVVVDGVRFP 16

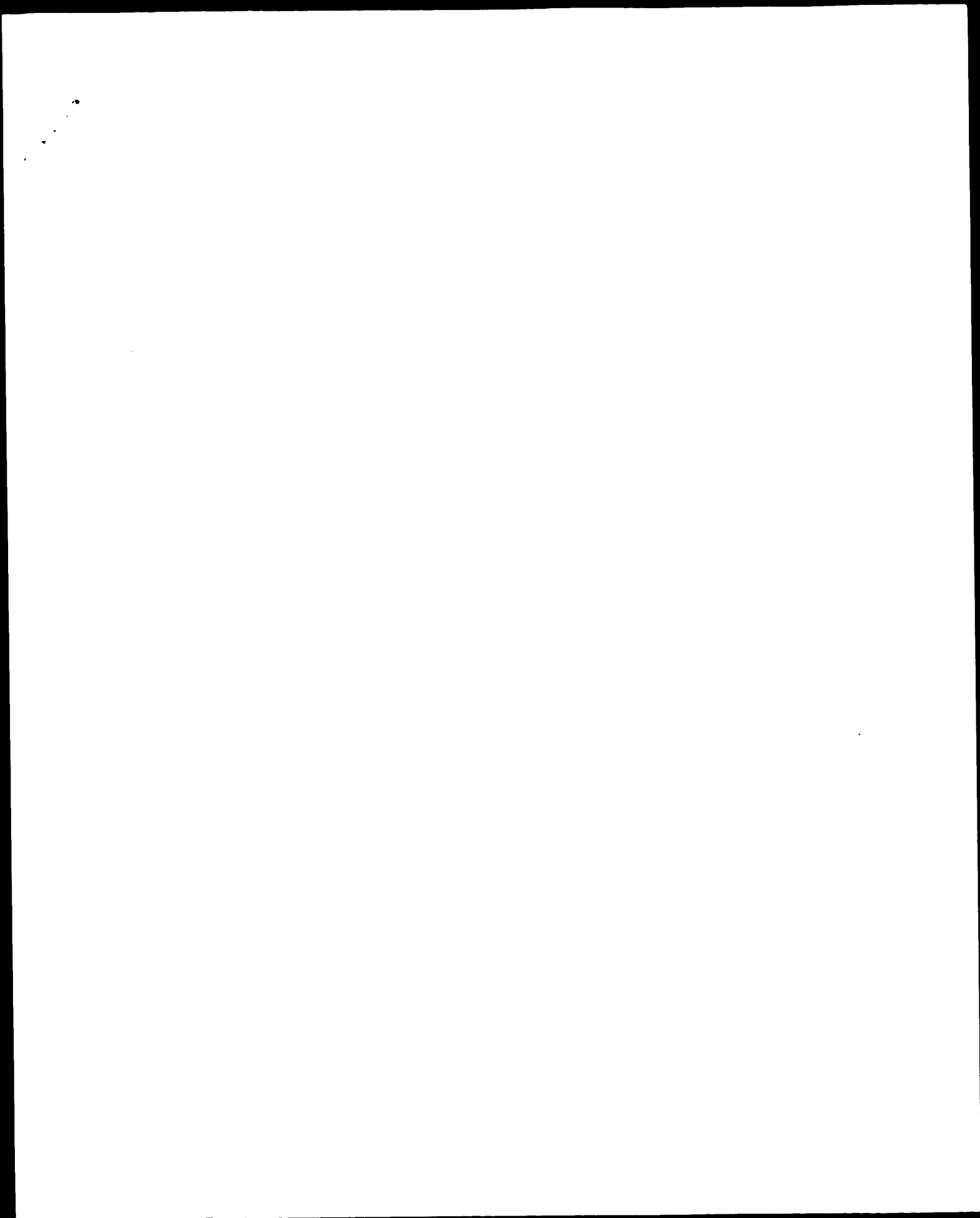
RESULT 15

O9SJA2 PRELIMINARY; PRT: 18 AA.
AC O9SJA2: 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE INTEGRIN ALPHA 2 SUBUNIT (FRAGMENT).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;

RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-CARDIOVASCULAR;
 RA Markmann A., Kresse H.;
 RT "Regulation of VSMC Differentiation."
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF330200; AAL09466.1; -
 FT NON_TER 1
 FT NON_TER 18
 SQ SEQUENCE 18 AA; 1944 MW; DFEAC6E14A5B0EF CRC64;

Query Match 19.18; Score 26; DB 6; Length 18;
 Best Local Similarity 50.0%; Pred. No. 3.9e+03;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 9 PKDIVRSI 16
 Db 4 PSDVNSL 11

Search completed: July 15, 2002, 12:53:42
 Job time: 198 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 15, 2002, 12:45:19 ; Search time 30.15 Seconds
(without alignments)
92.101 Million cell updates/sec

Title: US-09-938-700-4

Sequence: 1 CRVTHPLPRDIYRSIAKAPKRAP 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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3: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT:*
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18: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT:*
19: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT:*
20: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT:*
21: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:*
22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|---------------------|
| 1 | 136 | 100.0 | 124 | AAW24097 | Partial canine imm |
| 2 | 136 | 100.0 | 312 | AAW79995 | Dog immunoglobulin |
| 3 | 136 | 100.0 | 417 | AAW23067 | Canine Ige heavy c |
| 4 | 136 | 100.0 | 426 | AAW7753 | Canine Ige. Canis |
| 5 | 120.5 | 88.6 | 341 | AAW6208 | Immunogenic peptid |
| 6 | 105 | 77.2 | 340 | AAW3663 | Rat Ige heavy chain |
| 7 | 102 | 75.0 | 20 | AAW24102 | Canine immunoglobi |
| 8 | 99.5 | 73.2 | 341 | AAW6206 | Immunogenic peptid |
| 9 | 95.5 | 70.2 | 342 | AAW6205 | Immunogenic peptid |
| 10 | 93.5 | 68.8 | 345 | AAW6207 | Immunogenic peptid |
| 11 | 89 | 65.4 | 17 | AAW50893 | Antibody 15A.2 bin |

| | | | | | |
|----|----|------|-----|----------|----------------------|
| 12 | 89 | 65.4 | 17 | AAW50894 | Antibody 15A.2 can |
| 13 | 89 | 65.4 | 25 | AAW79999 | Optimised Ige-CH3 |
| 14 | 89 | 65.4 | 45 | AAW80019 | Ige immunogenic pe |
| 15 | 89 | 65.4 | 45 | AAW80083 | Ige immunogenic pe |
| 16 | 89 | 65.4 | 46 | AAW80020 | Ige immunogenic pe |
| 17 | 89 | 65.4 | 57 | AAW80081 | Ige immunogenic pe |
| 18 | 89 | 65.4 | 62 | AAW80080 | Ige immunogenic pe |
| 19 | 89 | 65.4 | 63 | AAW80084 | Ige immunogenic pe |
| 20 | 88 | 64.7 | 313 | AAW79996 | Rat immunoglobulin |
| 21 | 88 | 63.2 | 130 | AAW85585 | Fe(epsilon) CH2-C |
| 22 | 86 | 63.2 | 190 | AAW85584 | Fe(epsilon) CH2-C |
| 23 | 86 | 63.2 | 201 | AAW85589 | Fe(epsilon) CH2-C |
| 24 | 86 | 63.2 | 218 | AAW85583 | Fe(epsilon) CH2-C |
| 25 | 86 | 63.2 | 222 | AAW65592 | Amino acid sequenc |
| 26 | 86 | 63.2 | 315 | AAW85589 | Fe(epsilon) CH2-C |
| 27 | 86 | 63.2 | 324 | AAW83559 | Fe(epsilon) CH2-C |
| 28 | 86 | 63.2 | 325 | AAW83582 | CH2 to CH4 of huma |
| 29 | 86 | 63.2 | 325 | AAW75225 | Human Ige Fc chain |
| 30 | 86 | 63.2 | 325 | AAW77241 | Human Ige Fc chain |
| 31 | 86 | 63.2 | 325 | AAW79994 | Human Ige Fc chain |
| 32 | 86 | 63.2 | 331 | AAW80362 | Human Ige heavy ch |
| 33 | 86 | 63.2 | 367 | AAW80291 | Interleukin-2/Ige |
| 34 | 86 | 63.2 | 428 | AAW42950 | Human Ige heavy ch |
| 35 | 86 | 63.2 | 493 | AAW40065 | Sequence of human |
| 36 | 86 | 58.8 | 209 | AAW90010 | Residues 340-547 o |
| 37 | 79 | 58.1 | 20 | AAW24103 | Canine immunoglobi |
| 38 | 79 | 58.1 | 110 | AAW33324 | Variant Ige - muta |
| 39 | 79 | 57.4 | 106 | AAW42620 | Human Ige Fc epsilon |
| 40 | 78 | 57.4 | 110 | AAW33304 | Ige Fc epsilon 3. |
| 41 | 78 | 57.4 | 110 | AAW33314 | Variant Ige - muta |
| 42 | 78 | 57.4 | 110 | AAW33315 | Variant Ige - muta |
| 43 | 78 | 57.4 | 110 | AAW33316 | Variant Ige - muta |
| 44 | 78 | 57.4 | 110 | AAW33318 | Variant Ige - muta |
| 45 | 78 | 57.4 | 110 | AAW33319 | Variant Ige - muta |

ALIGNMENTS

RESULT 1
ID AAW24097 standard: peptide: 124 AA.
AAW24097;
AC AAW24097;
DT 21-NOV-1997 (first entry)
XX
DE Partial canine immunoglobulin E protein.
XX
KW Immunoglobulin E; Ige: anti-canine Ige antibody; allergy; canine; dog.
XX
OS Canis familiaris.
XX
PN JP09169795-A.
XX
PD 30-JUN-1997.
XX
PF 22-DEC-1995; 95JP-0334381.
XX
PR 22-DEC-1995; 95JP-0334381.
XX
PA (HITB) HITACHI CHDM CO LTD.
XX
DR WPI: 1997-389423/36.
XX
PS N-PSDB: AAT85646.
XX
PT Canine immunoglobulin E peptide fragment and related DNA - useful
XX for the preparation of anti-canine immunoglobulin E antibody
XX
PS Claim 1; Page 8; 12pp: Japanese.
XX
CC This is a partial canine immunoglobulin E (Ige) protein. Peptide
fragments (AAW24098-106) containing at least five continuous amino acids

CC of this sequence are used for the preparation of anti-canine IgE
 CC antibody. The anti-canine IgE antibody can be used for the diagnosis of
 CC canine allergies.

XX Sequence 124 AA;

Query Match 100.0%; Score 136; DB 18; Length 124;
 Best Local Similarity 100.0%; Pred. No. 2.6e-13;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRVTHPLPKDIVRSIAKAPGKRAP 25
 |||||
 Db 62 crvthplpkdivrsiakapgkrap 86

RESULT 2

ID AAY79995 standard; Protein: 312 AA.

AC AAY79995;

DT 15-MAY-2000 (first entry)

DE Dog immunoglobulin E epsilon heavy chain SEQ ID NO:2.

KW Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
 KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
 KW antibody; allergy; allergic disease; immunisation; anti-allergic;
 KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

OS Canis sp.

PN WO967293-A1.

PD 29-DEC-1999.

PF 21-JUN-1999; 99WO-US3959.

PR 20-JUN-1998; 98US-0100287.

PA (UNBI-) UNITED BIOMEDICAL INC.

PI Wang CY, Wallfield AM;

DR WPI: 2000-160578/14.

PT New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
 PT for immunization against allergy -

PS Example 1; Page 66-68; 155pp; English.

CC The present invention describes immunoglobulin E (IgE)-CH3 domain
 CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
 CC and anti-asthmatic properties. (I) induces polyclonal antibodies
 CC specific for a target effector site on the epsilon-heavy chain of IgE,
 CC and so preventing triggering and activation of mast cells and basophils
 CC and downregulation of IgE synthesis. Conjugates, or fusion peptides
 CC containing (I) are used for active immunisation against IgE-mediated
 CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
 CC dermatitis. Nucleic acids that encode these compounds are useful for
 CC recombinant production of corresponding peptides or in DNA vaccines.
 CC Conjugates of (I) that include a promiscuous T helper cell epitope
 CC (functional in genetically diverse subjects), in addition to a B cell
 CC target epitope, have increased immunogenicity and may include cyclic
 CC constraints (disulfide bridge) to stabilise conformational features and
 CC maximize cross-reactivity to the natural target. They induce safe
 CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino
 CC acid sequences used in the exemplification of the present invention.

XX Sequence 312 AA;

Query Match 100.0%; Score 136; DB 21; Length 312;
 Best Local Similarity 100.0%; Pred. No. 7.4e-13;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRVTHPLPKDIVRSIAKAPGKRAP 25
 |||||
 Db 192 crvthplpkdivrsiakapgkrap 216

RESULT 3

ID AAY23067 standard; Protein: 417 AA.

AC AAY23067;

DT 19-FEB-1998 (first entry)

DE Canine IgE heavy chain constant region (exon 1-4 product).

KW IgE; immunoglobulin; antibody; heavy chain constant region;
 KW allergy; hypersensitivity; therapy; dog; antisense;
 KW immunomodulation.

OS Canis familiaris.

PN Key Location/Qualifiers

FT Misc-difference 55 /note= "encoded by ACC"

FT Misc-difference 56 /note= "encoded by TAC"

FT Misc-difference 67 /note= "encoded by GCC"

FT Misc-difference 83 /note= "encoded by NNT"

FT Misc-difference 174 /note= "encoded by GGN"

FT Misc-difference 175 /note= "encoded by NNG"

FT Misc-difference 176 /note= "encoded by TGN"

FT Misc-difference 203 /note= "encoded by TCC"

FT Misc-difference 204 /note= "encoded by GAC"

PN WO9730156-A2.

PD 21-AUG-1997.

PF 14-FEB-1997; 97WO-US02322.

PR 14-FEB-1996; 96US-0601197.

PA (IDEXX-) IDEXX LAB INC.

PI Harris RA, Mermer B, Siefling AB;

DR WPI: 1997-425031/39.

DR N-PSDB: AAY79278.

PT Isolated canine IgE heavy chain constant region DNA - useful to
 PT develop products for treatment of canine allergies and for
 PT immunomodulation in dogs

PS Disclosure; Page 35-39; 59pp; English.

CC This polypeptide is encoded by exons 1-4 (see AAY79278) of canine
 CC IgE heavy chain constant region (epsilon) genomic DNA. Another
 CC polypeptide, comprising the exon 5 and 6 product, is given in
 CC AAY23068. Recombinant peptides encoded by exons 1-6 can be
 CC produced in eukaryotic or prokaryotic cells. Such peptides,
 CC and antibodies raised against them, are used in methods to treat
 CC the manifestation of allergy in dogs, e.g. to treatment Type I

CC immediate hypersensitivity, and for immunomodulation.
 XX
 SQ Sequence 417 AA;

Query Match 100.0%; Score 136; DB 18; Length 417;
 Best Local Similarity 100.0%; Pred. No. 1e-12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CRVTHPHLPKDIVRSIAKAPGRAP 25
 |||||
 DB 289 crvthphlpkdivrsiakapgrap 313

RESULT 4

AAR97753
 ID AAR97753 standard; Protein; 426 AA.
 XX
 AC AAR97753;
 XX
 DT 28-AUG-1996 (first entry)
 XX
 DE Canine Ige.
 XX
 KW Ige; immunoglobulin; antibody; vaccine; allergy; hypersensitivity.
 XX
 OS Canis familiaris.
 XX
 PN WO9614867-A1.
 XX
 PD 23-MAY-1996.
 XX
 PF 03-NOV-1995; 95WO-US13795.
 XX
 PR 09-NOV-1994; 94US-0336891.
 PR 09-NOV-1994; 94US-0336583.
 XX
 PA (MERI) MERCK & CO INC.
 XX
 PI Hollis GF, Patel MD;
 XX
 DR WPI; 1996-277321/28.
 DR N-PSDB; AAT29824.
 XX
 PT New DNA encoding canine Ige and Iga - useful in vaccines, antisense
 PT therapy, assays, drug screening, etc.
 XX
 PS Claim 11; Page 29-30; 49pp; English.
 XX
 CC The canine Ige amino acid sequence (AAR97753) was deduced from
 CC an isolated gene (AAT29824) obt'd. from a canine liver DNA library.
 CC The cloning of the Ige gene allows prodn. of large quantities of
 CC recombinant Ige using bacterial, yeast, mammalian, insect or
 CC viral systems. The Ige can be used in drug development (e.g.
 CC small molecule screening, assay development and anti-Ige
 CC antibody generation). Fragments of Ige can be used in vaccines
 CC or to prevent Ige-mediated hypersensitivity. The new sequence
 CC information permits targeted modulation of Ige-mediated immune
 CC responses.
 CC
 SQ Sequence 426 AA;

Query Match 100.0%; Score 136; DB 17; Length 426;
 Best Local Similarity 100.0%; Pred. No. 1.1e-12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRVTHPHLPKDIVRSIAKAPGRAP 25
 |||||
 DB 294 crvthphlpkdivrsiakapgrap 318

RESULT 5

AAB06208
 ID AAB06208 standard; protein; 341 AA.
 XX
 AC AAB06208;
 XX
 DT 22-NOV-2000 (first entry)
 XX
 DE Immunogenic peptide consisting of opossum CH2, dog CH3 and opossum CH4.
 XX
 KW Dog; opossum; immunoglobulin E; Ige; vaccination; infection; allergy;
 KW asthma; eczema; immunogenic peptide.
 XX
 OS Chimeric - Didelphis virginiana.
 XX
 PN WO200025722-A2.
 XX
 PD 11-MAY-2000.
 XX
 PF 21-OCT-1999; 99WO-SE01896.
 XX
 PR 02-NOV-1998; 98US-0106652.
 PR 22-SEP-1999; 99US-0401636.
 XX
 PA (RESI-) RESISTENTIA PHARM AB.
 XX
 PI Hellman LT;
 XX
 DR WPI; 2000-365342/31.
 XX
 PT Immunogenic polypeptides useful for preventing the harmful effects of
 PT immunoglobulin E in mammals -
 XX
 PS Disclosure; Fig 2; 50pp; English.
 XX
 CC The present sequence is an immunogenic peptide consisting of the heavy
 CC chain constant regions 2 and 4 of the opossum Ige and the heavy chain
 CC constant region 3 from the dog. It was shown to cause a stronger
 CC polyclonal anti-self Ige response than peptides consisting of the same
 CC regions from one mammal. Immunogenic peptides, particularly those
 CC consisting of different heavy chain constant regions, can be used for
 CC vaccination in humans, against bacterial and viral infections and
 CC allergies, such as asthma, fur, pollen and food allergies and eczema.
 CC
 SQ Sequence 341 AA;

Query Match 88.6%; Score 120.5; DB 21; Length 341;
 Best Local Similarity 92.3%; Pred. No. 2.1e-10;
 Matches 24; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 CRVTHPHLPKDIVRSIAKAPGRAP 25
 |||||
 DB 211 crvthphlpkdivrsiakapgrap 236

RESULT 6

AAB03643
 ID AAB03643 standard; protein; 340 AA.
 XX
 AC AAB03643;
 XX
 DT 22-NOV-2000 (first entry)
 XX
 DE Rat Ige heavy chain constant regions 2, 3 and 4.
 XX
 KW Rat; immunoglobulin E; Ige; vaccination; infection; allergy;
 KW asthma; eczema; immunogenic peptide.
 XX
 OS Rattus sp.
 XX
 PN WO200025722-A2.
 XX

PD 11-MAY-2000.
 XX
 PF 21-OCT-1999; 99WO-SE01896.
 XX
 PR 02-NOV-1998; 98US-0106652.
 PR 22-SEP-1999; 99US-0401636.
 XX
 PA (RESI-) RESISTENTIA PHARM AB.
 XX
 PI Hellman LT;
 PI
 DR WPI: 2000-365342/31.
 XX
 PT Immunogenic polypeptides useful for preventing the harmful effects of
 XX Immunoglobulin E in mammals -
 XX
 PS Disclosure; Fig 1; 50pp; English.
 XX
 CC The present sequence is an immunogenic peptide consisting of the
 CC heavy chain constant regions 2, 3 and 4 of the rat IGE. It was used to
 CC construct a number of immunogenic peptides which consisted of regions of
 CC IGE from different mammals, which appear to cause a stronger polyclonal
 CC anti-self IGE response than peptides consisting of the same regions from
 CC one mammal. Immunogenic peptides, particularly those consisting of
 CC different heavy chain constant regions, can be used for vaccination
 CC in humans, against bacterial and viral infections and allergies, such
 CC as asthma, fur, pollen and food allergies and eczema.
 CC
 SQ Sequence 340 AA;
 XX

Query Match 77.2%; Score 105; DB 21; Length 340;
 Best Local Similarity 79.2%; Pred. No. 5.1e-08;
 Matches 19; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 CRVTHPLPKDIVRSIAKAPGKRA 24
 DB 200 crvdhphfpxkplvrsitkpgkrs 223

RESULT 7
 AAW24102
 ID AAW24102 standard; peptide; 20 AA.
 XX
 AC AAW24102;
 XX
 DT 21-NOV-1997 (first entry)
 XX
 DE Canine immunoglobulin E peptide 5.
 XX
 KW Immunoglobulin E; IGE; anti-canine IGE antibody; allergy; canine; dog.
 XX
 OS Canis familiaris.
 XX
 PN JP09169795-A.
 XX
 PD 30-JUN-1997.
 XX
 PF 22-DEC-1995; 95JP-0334381.
 XX
 PR 22-DEC-1995; 95JP-0334381.
 XX
 PA (HITB) HITACHI CHEM CO LTD.
 XX
 DR WPI: 1997-389423/36.
 DR N-PSDB; AAT85651.
 XX
 PT Canine immunoglobulin E peptide fragment and related DNA - useful
 XX for the preparation of anti-canine immunoglobulin E antibody
 PS Claim 2; Page 9; 12pp; Japanese.
 XX
 CC AAW24098-106 are peptide fragments containing at least 5 continuous

CC amino acids of the partial canine immunoglobulin E (IGE) protein shown
 CC in AAW24097. The peptides are used for the preparation of anti-canine
 CC IGE antibody. The anti-canine IGE antibody can be used for the diagnosis
 CC of canine allergies.
 XX
 SQ Sequence 20 AA;
 XX

Query Match 75.0%; Score 102; DB 18; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.1e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CRVTHPLPKDIVRSIAKAPGKRA 19
 DB 2 crvdhphfpxkplvrsitkpgkrlap 20

RESULT 8
 AAB06206
 ID AAB06206 standard; protein; 341 AA.
 XX
 AC AAB06206;
 XX
 DT 22-NOV-2000 (first entry)
 XX
 DE Immunogenic peptide consisting of opossum CH2, rat CH3 and opossum CH4.
 XX
 KW Rat; Opossum; immunoglobulin E; IGE; vaccination; infection; allergy;
 KW asthma; eczema; immunogenic peptide.
 XX
 OS Chimeric - Didelphis virginiana.
 OS Chimeric - Rattus sp.
 XX
 PN WO200025722-A2.
 XX
 PD 11-MAY-2000.
 XX
 PF 21-OCT-1999; 99WO-SE01896.
 XX
 PR 02-NOV-1998; 98US-0106652.
 PR 22-SEP-1999; 99US-0401636.
 XX
 PA (RESI-) RESISTENTIA PHARM AB.
 XX
 PI Hellman LT;
 PI
 DR WPI: 2000-365342/31.
 XX
 PT Immunogenic polypeptides useful for preventing the harmful effects of
 XX Immunoglobulin E in mammals -
 XX
 PS Disclosure; Fig 2; 50pp; English.
 XX
 CC The present sequence is an immunogenic peptide consisting of the heavy
 CC chain constant regions 2 and 4 of the opossum IGE and the heavy chain
 CC constant region 3 from the rat. It was shown to cause a stronger
 CC polyclonal anti-self IGE response than peptides consisting of the same
 CC regions from one mammal. Immunogenic peptides, particularly those
 CC consisting of different heavy chain constant regions, can be used for
 CC vaccination in humans, against bacterial and viral infections and
 CC allergies, such as asthma, fur, pollen and food allergies and eczema.
 CC
 SQ Sequence 341 AA;
 XX

Query Match 73.2%; Score 99.5; DB 21; Length 341;
 Best Local Similarity 76.9%; Pred. No. 3.7e-07;
 Matches 20; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
 QY 1 CRVTHPLPKDIVRSIAKAPGKRA-AP 25
 DB 211 crvdhphfpxkplvrsitkpgkrlap 236


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RESULT 9
AAB06205
ID AAB06205 standard; protein; 342 AA.
XX
AC AAB06205;
XX
DT 22-NOV-2000 (first entry)
XX
DE Immunogenic peptide consisting of opossum CH2, human CH3 and opossum CH4.
XX
KM Human; opoosum; immunoglobulin E; IgE; vaccination; infection; allergy;
XX
KM asthma; eczema; immunogenic peptide.
XX
OS Chimeric - Didelphis virginiana.
XX
OS Chimeric - Homo sapiens.
XX
PN WO200025722-A2.
XX
PD 11-MAY-2000.
XX
PF 21-OCT-1999; 99WO-SE01896.
XX
PR 02-NOV-1998; 98US-0106652.
XX
PR 22-SEP-1999; 99US-0401636.
XX
PA (RESI-) RESISTENTIA PHARM AB.
XX
PI Helman LT;
XX
DR WPI; 2000-365342/31.
XX
PT Immunogenic polypeptides useful for preventing the harmful effects of
XX immunoglobulin E in mammals -
XX
PS Disclosure; Fig 2; 50pp; English.
XX
CC The present sequence is an immunogenic peptide consisting of the heavy
CC chain constant regions 2 and 4 of the opossum IgE and the heavy chain
CC constant region 3 from the human. It was shown to cause a stronger
CC polyclonal anti-self IgE response than peptides consisting of the same
CC regions from one mammal. Immunogenic peptides, particularly those
CC consisting of different heavy chain constant regions, can be used for
CC vaccination in humans, against bacterial and viral infections and
CC allergies, such as asthma, fur, pollen and food allergies and eczema.
XX
SQ Sequence 342 AA;

Query Match 70.2%; Score 95.5; DB 21; Length 342;
Best Local Similarity 69.2%; Pred. No. 1.5e-06;
Matches 18; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

QY 1 CRVTHPLPKDVIKSIKAPGR-AP 25
DB 212 crvthplpkdvlrsklpgkrlap 237

RESULT 10
AAB06207
ID AAB06207 standard; protein; 345 AA.
XX
AC AAB06207;
XX
DT 22-NOV-2000 (first entry)
XX
DE Immunogenic peptide consisting of opossum CH2, pig CH3 and opossum CH4.
XX
KM Pig; opoosum; immunoglobulin E; IgE; vaccination; infection; allergy;
XX
KM asthma; eczema; immunogenic peptide.
XX
OS Chimeric - Didelphis virginiana.
OS Chimeric - Sus scrofa.

```

```

XX
PN WO200025722-A2.
XX
PD 11-MAY-2000.
XX
PF 21-OCT-1999; 99WO-SE01896.
XX
PR 02-NOV-1998; 98US-0106652.
XX
PR 22-SEP-1999; 99US-0401636.
XX
PA (RESI-) RESISTENTIA PHARM AB.
XX
PI Helman LT;
XX
DR WPI; 2000-365342/31.
XX
PT Immunogenic polypeptides useful for preventing the harmful effects of
XX immunoglobulin E in mammals -
XX
PS Disclosure; Fig 2; 50pp; English.
XX
CC The present sequence is an immunogenic peptide consisting of the heavy
CC chain constant regions 2 and 4 of the opossum IgE and the heavy chain
CC constant region 3 from the pig. It was shown to cause a stronger
CC polyclonal anti-self IgE response than peptides consisting of the same
CC regions from one mammal. Immunogenic peptides, particularly those
CC consisting of different heavy chain constant regions, can be used for
CC vaccination in humans, against bacterial and viral infections and
CC allergies, such as asthma, fur, pollen and food allergies and eczema.
XX
SQ Sequence 345 AA;

Query Match 68.8%; Score 93.5; DB 21; Length 345;
Best Local Similarity 73.1%; Pred. No. 3.1e-06;
Matches 19; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

QY 1 CRVTHPLPKDVIKSIKAPGR-AP 25
DB 215 crvthplpkdvlrsklpgkrlap 240

RESULT 11
AAV50893
ID AAV50893 standard; peptide; 17 AA.
XX
AC AAV50893;
XX
DT 24-FEB-2000 (first entry)
XX
DE Antibody 15A.2 binding peptide 10 from PhdC7c phage display library.
XX
KM Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy;
XX epitope; prophylaxis; treatment; minotope.
XX
OS Synthetic.
XX
PN EP957111-A2.
XX
PD 17-NOV-1999.
XX
PF 09-APR-1999; 99EP-0107035.
XX
PR 09-APR-1998; 98US-0058331.
XX
PR 30-MAR-1999; 99US-0281760.
XX
PA (IDEX-) IDEXX LAB INC.
XX
PI Lawton R, Mermer B, Francoeur G;
XX
DR WPI; 2000-040833/04.
XX
PT Binding proteins used for treatment or prophylaxis of canine allergy -

```

XX Disclosure; Fig 6; 30pp; English.
 PS
 CC This invention describes a novel binding protein which specifically
 CC binds to native canine free or B-cell bound IgE, and which doesn't bind
 CC to IgE when the IgE is bound to mast cells. The peptide products of the
 CC invention have anti-allergic activity. The antibodies bind to defined
 CC epitopes on free or B-cell bound IgE molecules which have an important
 CC role in allergic reaction. The specific binding proteins are used to
 CC produce a pharmaceutical composition, preferably with a diluent, which
 CC can be used for prophylaxis or treatment of canine allergy.
 CC AAY50876-Y50900 represent peptide mimotopes used in the method of the
 CC invention.
 CC
 SQ Sequence 17 AA;

Query Match 65.4%; Score 89; DB 21; Length 17;
 Best Local Similarity 100.0%; Pred. No. 5.2e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CRVTHPHLPKDIVRSI 16
 ||||||||||||||||
 DB 2 crvthphlpkdivrsi 17

RESULT 12

AAY50894
 ID AAY50894 standard; peptide; 17 AA.

AC AAY50894;

DT 24-FEB-2000 (first entry)

DE Antibody 15A.2 canine IgE binding epitope 1.

KW Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy;
 KW epitope; prophylaxis; treatment; mimotope.

OS Synthetic.

PN EP957111-A2.

PD 17-NOV-1999.

PE 09-APR-1999; 99EP-0107035.

PR 09-APR-1998; 98US-0058331.

PR 30-MAR-1999; 99US-0281760.

PA (IDEX-) IDEXX LAB INC.

PI Lawton R, Mermer B, Francoeur G;

DR WPI: 2000-040833/04.

XX Binding proteins used for treatment or prophylaxis of canine allergy -
 PT
 PS disclosure; Fig 7; 30pp; English.

XX This invention describes a novel binding protein which specifically
 CC binds to native canine free or B-cell bound IgE, and which doesn't bind
 CC to IgE when the IgE is bound to mast cells. The peptide products of the
 CC invention have anti-allergic activity. The antibodies bind to defined
 CC epitopes on free or B-cell bound IgE molecules which have an important
 CC role in allergic reaction. The specific binding proteins are used to
 CC produce a pharmaceutical composition, preferably with a diluent, which
 CC can be used for prophylaxis or treatment of canine allergy.
 CC AAY50876-Y50900 represent peptide mimotopes used in the method of the
 CC invention.
 CC
 SQ Sequence 17 AA;

Query Match 65.4%; Score 89; DB 21; Length 17;
 Best Local Similarity 100.0%; Pred. No. 5.2e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CRVTHPHLPKDIVRSI 16
 ||||||||||||||||
 DB 2 crvthphlpkdivrsi 17

RESULT 13

AAY79999
 ID AAY79999 standard; Peptide; 25 AA.

AC AAY79999;

DT 15-MAY-2000 (first entry)

DE Optimised IgE-CH3 domain antigen peptide for dog IgE.

KW Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;

KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
 KW antibody; allergy; allergic disease; immunisation; anti-allergic;
 KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

OS Canis sp.
 OS Synthetic.

PN W09967293-A1.

PD 29-DEC-1999.

PE 21-JUN-1999; 99MO-US13959.

PR 20-JUN-1998; 98US-0100287.

PA (UNBI-) UNITED BIOMEDICAL INC.

PI Wang CY, Walfield AM;

DR WPI: 2000-160578/14.

XX New antigenic peptide from the CH3 domain of Immunoglobulin E, fusions
 PT for immunization against allergy -

PS Claim 1; Page 99; 155pp; English.

XX The present invention describes immunoglobulin E (IgE)-CH3 domain
 CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
 CC and anti-asthmatic properties. (I) induces polyclonal antibodies
 CC specific for a target effector site on the epsilon-heavy chain of IgE,
 CC and so preventing triggering and activation of mast cells and basophils
 CC and downregulation of IgE synthesis. Conjugates, or fusion peptides,
 CC containing (I) are used for active immunisation against IgE-mediated
 CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
 CC dermatitis. Nucleic acids that encode these compounds are useful for
 CC recombinant production of corresponding peptides or in DNA vaccines.
 CC Conjugates of (I) that include a promiscuous T helper cell epitope
 CC (functional in genetically diverse subjects), in addition to a B cell
 CC target epitope, have increased immunogenicity and may include cyclic
 CC constraints (disulfide bridge) to stabilise conformational features and
 CC maximize cross-reactivity to the natural target. They induce safe
 CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino
 CC acid sequences used in the exemplification of the present invention.
 CC
 SQ Sequence 25 AA;

Query Match 65.4%; Score 89; DB 21; Length 25;
 Best Local Similarity 100.0%; Pred. No. 8e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 RVTTHPHLPKDIVRSIAK 18

Db 8 rvtphlpkdivrsiak 24

RESULT 14

ID AAY80019 standard; Peptide: 45 AA.

AC AAY80019;

DE 15-MAY-2000 (first entry)

OS IGE immunogenic peptide conjugate SEQ ID NO:26.

Immunoglobulin E; IGE; epsilon heavy chain; antigenic; antigen;
immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
antibody; allergy; allergic disease; immunisation; anti-allergic;
anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

OS Unidentified.

PN MO9967293-A1.

PD 29-DEC-1999.

PF 21-JUN-1999; 99WO-US13959.

PR 20-JUN-1998; 98US-0100287.

PA (UNBI-) UNITED BIOMEDICAL INC.

PI Wang CY, Walfield AM;

WPI; 2000-160578/14.

New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
for immunization against allergy -

Claim 14; Page 76; 155pp; English.

The present invention describes immunoglobulin E (IGE)-CH3 domain
antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
and anti-asthmatic properties. (I) induces polyclonal antibodies
specific for a target effector site on the epsilon-heavy chain of IGE,
and so preventing triggering and activation of mast cells and basophils
containing (I) are used for active immunisation against IGE-mediated
allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
dermatitis. Nucleic acids that encode these compounds are useful for
recombinant production of corresponding peptides or in DNA vaccines.
Conjugates of (I) that include a promiscuous T helper cell epitope
(functional in genetically diverse subjects), in addition to a B cell
target epitope, have increased immunogenicity and may include cyclic
constraints (disulfide bridge) to stabilise conformational features and
maximize cross-reactivity to the natural target. They induce safe
acid sequences used in the exemplification of the present invention.

Sequence 45 AA:

Query Match 65.4%; Score 89; DB 21; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RYTHPHLPKDIVRSIAK 18

Db 28 rvtphlpkdivrsiak 44

RESULT 15
AAY80083
ID AAY80083 standard; Peptide: 45 AA.

AC AAY80083;

DE 15-MAY-2000 (first entry)

OS IGE immunogenic peptide conjugate SEQ ID NO:90.

Immunoglobulin E; IGE; epsilon heavy chain; antigenic; antigen;
immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
antibody; allergy; allergic disease; immunisation; anti-allergic;
anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

OS Unidentified.

PN MO9967293-A1.

PD 29-DEC-1999.

PF 21-JUN-1999; 99WO-US13959.

PR 20-JUN-1998; 98US-0100287.

PA (UNBI-) UNITED BIOMEDICAL INC.

PI Wang CY, Walfield AM;

WPI; 2000-160578/14.

New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
for immunization against allergy -

Claim 14; Page 77; 155pp; English.

The present invention describes immunoglobulin E (IGE)-CH3 domain
antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
and anti-asthmatic properties. (I) induces polyclonal antibodies
specific for a target effector site on the epsilon-heavy chain of IGE,
and so preventing triggering and activation of mast cells and basophils
containing (I) are used for active immunisation against IGE-mediated
allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
dermatitis. Nucleic acids that encode these compounds are useful for
recombinant production of corresponding peptides or in DNA vaccines.
Conjugates of (I) that include a promiscuous T helper cell epitope
(functional in genetically diverse subjects), in addition to a B cell
target epitope, have increased immunogenicity and may include cyclic
constraints (disulfide bridge) to stabilise conformational features and
maximize cross-reactivity to the natural target. They induce safe
acid sequences used in the exemplification of the present invention.

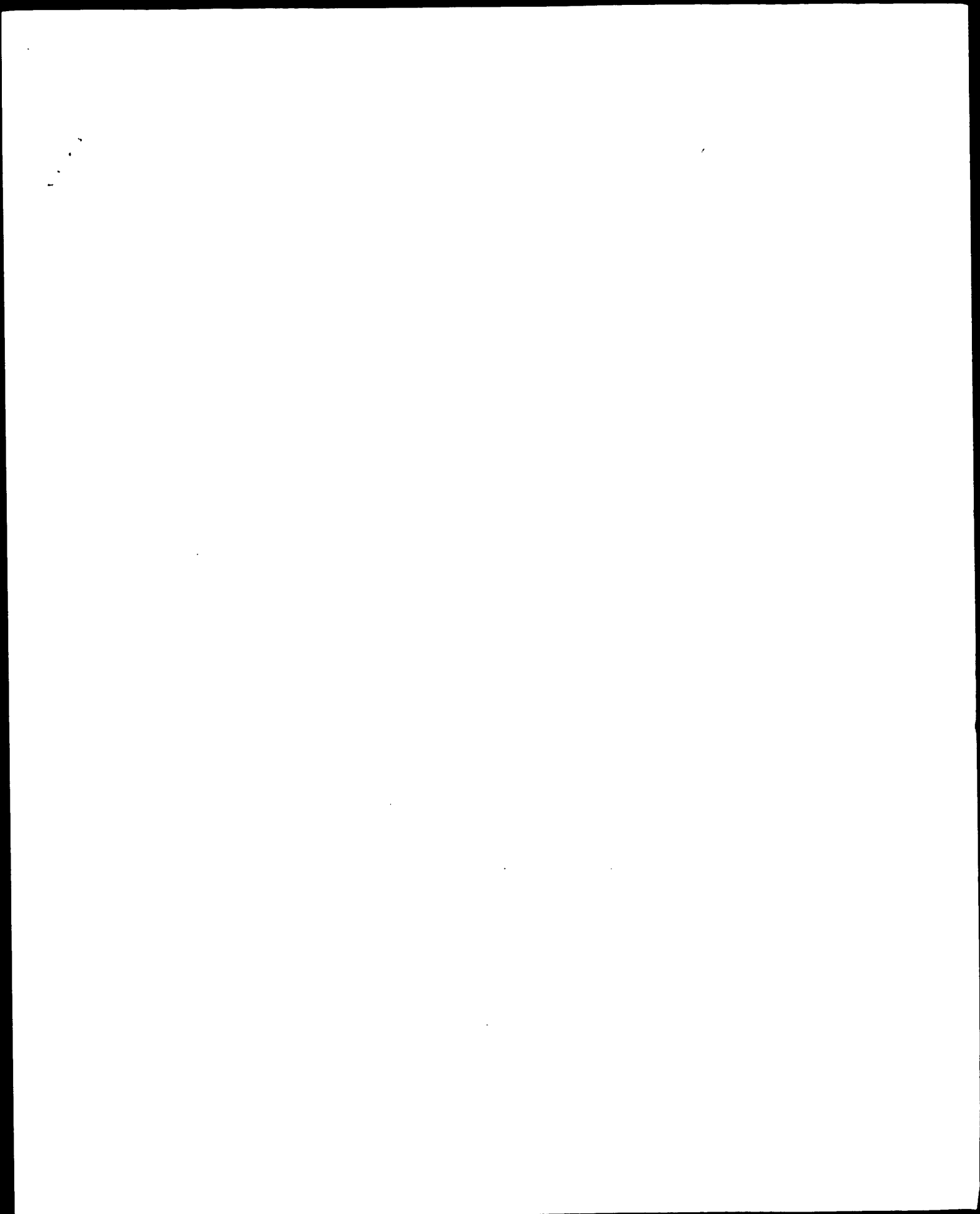
Sequence 45 AA:

Query Match 65.4%; Score 89; DB 21; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RYTHPHLPKDIVRSIAK 18

Db 28 rvtphlpkdivrsiak 44

Search completed: July 15, 2002, 12:46:17
Job time: 58 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 15, 2002, 12:45:19 ; Search time 12.97 Seconds

(without alignments)
47.081 Million cell updates/sec

Title: US-09-938-700-4

Perfect score: 136

Sequence: 1 CRVTHPLPKDIVRSIAKAPGKRAP 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

231628

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued_Patents_AA.*

2: /cgn2_6/ptodata/2/1aa/5A.COMB.pep.*

3: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*

4: /cgn2_6/ptodata/2/1aa/6A.COMB.pep.*

5: /cgn2_6/ptodata/2/1aa/6B.COMB.pep.*

6: /cgn2_6/ptodata/2/1aa/6C.COMB.pep.*

7: /cgn2_6/ptodata/2/1aa/6D.COMB.pep.*

8: /cgn2_6/ptodata/2/1aa/6E.COMB.pep.*

9: /cgn2_6/ptodata/2/1aa/6F.COMB.pep.*

10: /cgn2_6/ptodata/2/1aa/6G.COMB.pep.*

11: /cgn2_6/ptodata/2/1aa/6H.COMB.pep.*

12: /cgn2_6/ptodata/2/1aa/6I.COMB.pep.*

13: /cgn2_6/ptodata/2/1aa/6J.COMB.pep.*

14: /cgn2_6/ptodata/2/1aa/6K.COMB.pep.*

15: /cgn2_6/ptodata/2/1aa/6L.COMB.pep.*

16: /cgn2_6/ptodata/2/1aa/6M.COMB.pep.*

17: /cgn2_6/ptodata/2/1aa/6N.COMB.pep.*

18: /cgn2_6/ptodata/2/1aa/6O.COMB.pep.*

19: /cgn2_6/ptodata/2/1aa/6P.COMB.pep.*

20: /cgn2_6/ptodata/2/1aa/6Q.COMB.pep.*

21: /cgn2_6/ptodata/2/1aa/6R.COMB.pep.*

22: /cgn2_6/ptodata/2/1aa/6S.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | DB | ID | Description |
|------------|-------|-------|--------|----|--------------------|--------------------|
| 1 | 136 | 100.0 | 426 | 1 | US-08-336-583-2 | Sequence 2, Appl |
| 2 | 136 | 100.0 | 426 | 1 | PCT-US95-13795-2 | Sequence 2, Appl |
| 3 | 78 | 57.4 | 106 | 2 | US-08-232-539D-54 | Sequence 54, Appl |
| 4 | 78 | 57.4 | 109 | 4 | US-08-466-163B-1 | Sequence 1, Appl |
| 5 | 78 | 57.4 | 113 | 2 | US-08-232-539D-56 | Sequence 56, Appl |
| 6 | 67.5 | 49.6 | 118 | 3 | US-08-466-151-1 | Sequence 1, Appl |
| 7 | 67.5 | 49.6 | 119 | 2 | US-08-466-025A-1 | Sequence 1, Appl |
| 8 | 64 | 47.1 | 25 | 3 | US-09-100-414B-95 | Sequence 95, Appl |
| 9 | 64 | 47.1 | 25 | 3 | US-09-303-323-95 | Sequence 95, Appl |
| 10 | 64 | 47.1 | 25 | 3 | US-09-100-414B-98 | Sequence 98, Appl |
| 11 | 64 | 47.1 | 42 | 3 | US-09-100-414B-99 | Sequence 99, Appl |
| 12 | 64 | 47.1 | 42 | 3 | US-09-100-414B-100 | Sequence 100, Appl |
| 13 | 64 | 47.1 | 42 | 4 | US-09-303-323-98 | Sequence 98, Appl |
| 14 | 64 | 47.1 | 42 | 4 | US-09-303-323-99 | Sequence 99, Appl |
| 15 | 64 | 47.1 | 42 | 4 | US-09-303-323-100 | Sequence 100, Appl |
| 16 | 64 | 47.1 | 45 | 4 | US-09-100-414B-101 | Sequence 101, Appl |
| 17 | 64 | 47.1 | 45 | 4 | US-09-303-323-101 | Sequence 101, Appl |
| 18 | 64 | 47.1 | 46 | 3 | US-09-100-414B-96 | Sequence 96, Appl |
| 19 | 64 | 47.1 | 46 | 3 | US-09-100-414B-97 | Sequence 97, Appl |
| 20 | 64 | 47.1 | 46 | 4 | US-09-303-323-96 | Sequence 96, Appl |
| 21 | 64 | 47.1 | 63 | 4 | US-09-303-323-97 | Sequence 97, Appl |
| 22 | 64 | 47.1 | 63 | 4 | US-09-100-414B-102 | Sequence 102, Appl |
| 23 | 64 | 47.1 | 63 | 3 | US-09-303-323-102 | Sequence 102, Appl |
| 24 | 60 | 44.1 | 22 | 2 | US-08-232-539D-19 | Sequence 19, Appl |
| 25 | 60 | 44.1 | 22 | 2 | US-08-232-539D-20 | Sequence 20, Appl |
| 26 | 60 | 44.1 | 56 | 2 | US-08-232-539D-18 | Sequence 18, Appl |
| 27 | 58 | 42.6 | 331 | 2 | US-08-646-981-17 | Sequence 17, Appl |

| | | | | | | |
|----|------|------|------|---|-------------------|-------------------|
| 28 | 54 | 39.7 | 1886 | 4 | US-08-938-105-3 | Sequence 3, Appl |
| 29 | 54 | 39.7 | 1939 | 4 | US-09-310-187A-1 | Sequence 1, Appl |
| 30 | 51 | 37.5 | 467 | 2 | US-07-916-098A-45 | Sequence 45, Appl |
| 31 | 50.5 | 37.1 | 326 | 3 | US-08-808-720-3 | Sequence 3, Appl |
| 32 | 50.5 | 37.1 | 327 | 2 | US-08-761-277A-47 | Sequence 47, Appl |
| 33 | 50.5 | 37.1 | 328 | 3 | US-08-808-720-1 | Sequence 1, Appl |
| 34 | 50.5 | 37.1 | 331 | 3 | US-08-808-720-5 | Sequence 5, Appl |
| 35 | 50.5 | 37.1 | 331 | 3 | US-08-808-720-7 | Sequence 7, Appl |
| 36 | 50.5 | 37.1 | 337 | 3 | US-08-808-720-7 | Sequence 7, Appl |
| 37 | 50.5 | 37.1 | 357 | 3 | US-08-630-172-20 | Sequence 20, Appl |
| 38 | 50.5 | 37.1 | 367 | 3 | US-09-375-419-20 | Sequence 19, Appl |
| 39 | 50.5 | 37.1 | 367 | 4 | US-09-375-419-19 | Sequence 19, Appl |
| 40 | 50.5 | 37.1 | 378 | 3 | US-08-630-172-21 | Sequence 21, Appl |
| 41 | 50.5 | 37.1 | 378 | 4 | US-09-375-419-21 | Sequence 21, Appl |
| 42 | 50.5 | 37.1 | 382 | 1 | US-08-470-289-7 | Sequence 7, Appl |
| 43 | 50.5 | 37.1 | 382 | 1 | US-08-470-289-10 | Sequence 10, Appl |
| 44 | 50.5 | 37.1 | 386 | 4 | US-08-875-533-42 | Sequence 42, Appl |
| 45 | 50.5 | 37.1 | 392 | 4 | US-08-875-533-41 | Sequence 41, Appl |

ALIGNMENTS

RESULT 1
US-08-336-583-2
Sequence 2, Application US/08336583
Patent No. 5629415
GENERAL INFORMATION:
APPLICANT: HOLLIS, GREGORY F.
APPLICANT: PATEL, MAYUR D.
TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULIN E
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHRISTINE E. CARTY
STREET: 126 E. LINCOLN AVENUE
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,583
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 19211
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-6734
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 426 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-336-583-2

Query Match 100.0%: Score 136; DB 1: Length 426;
Best Local Similarity 100.0%: Pred. No. 1.9e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CRVTHPLPKDIVRSIAKAPGKRAP 25
|||||
DB 294 CRVTHPLPKDIVRSIAKAPGKRAP 318

RESULT 2
PCT-US95-13795-2
Sequence 2 Application PC/TUS9513795
GENERAL INFORMATION:
APPLICANT: HOLTS, GREGORY F.
APPLICANT: PATEL, MAYUR D.
TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: CHRISTINE E. CARTY
STREET: 126 E. LINCOLN AVENUE; P.O. BOX 2000
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13795
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 19211Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-6734
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 426 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-13795-2

Query Match 100.0%; Score 136; DB 5; Length 426;
Best Local Similarity 100.0%; Pred. No. 1.9e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRYTHRHPKDIVRSIAKAPGRAP 25
DB 294 CRYTHRHPKDIVRSIAKAPGRAP 318

RESULT 3
US-08-232-539D-54
Sequence 54, Application US/08232539D
Patent No. 5965709
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: 19E Antagonists
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/232,539D
FILING DATE: 21-Apr-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/178583
FILING DATE: 07-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/744768
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Syvoda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P0718P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: Amino acid
TOPOLOGY: Linear
US-08-232-539D-54

Query Match 57.4%; Score 78; DB 2; Length 106;
Best Local Similarity 61.9%; Pred. No. 4.3e-05;
Matches 13; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 CRYTHRHPKDIVRSIAKAPG 21
DB 84 CRYTHRHPKDIVRSIAKAPG 104

RESULT 4
US-08-466-163B-1
Sequence 1, Application US/08466163B
Patent No. 6329509
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: Immunoglobulin Variants
FILE REFERENCE: P0718P2C1D1
CURRENT APPLICATION NUMBER: US/08/466,163B
CURRENT FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR FILING DATE: 1995-03-15
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR FILING DATE: 1994-01-26
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR FILING DATE: 1992-05-07
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR FILING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 64
SEQ ID NO 1
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
US-08-466-163B-1

Query Match 57.4%; Score 78; DB 4; Length 109;
Best Local Similarity 61.9%; Pred. No. 4.3e-05;
Matches 13; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 CRYTHRHPKDIVRSIAKAPG 21
DB 88 CRYTHRHPKDIVRSIAKAPG 108

RESULT 5
US-08-232-539D-56
Sequence 56, Application US/08232539D
Patent No. 5965709

REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-100-414B-98

Query Match 47.1%; Score 64; DB 3; Length 42;
Best Local Similarity 64.7%; Pred. No. 0.0023;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 RYTHPHLPKDIVRSIAK 18
Db 25 RYTHPHLPRAIMRSTTK 41

RESULT 11
US-09-100-414B-99
Sequence 99, Application US/09100414B
Patent No. 6025468
GENERAL INFORMATION:
APPLICANT: Wang, Chang YI
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,414B
FILING DATE: 20-JUNE-1998
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-100-414B-99

Query Match 47.1%; Score 64; DB 3; Length 42;
Best Local Similarity 64.7%; Pred. No. 0.0023;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 RYTHPHLPKDIVRSIAK 18
Db 25 RYTHPHLPRAIMRSTTK 41

RESULT 12
US-09-100-414B-100
Sequence 100, Application US/09100414B
Patent No. 6025468
GENERAL INFORMATION:
APPLICANT: Wang, Chang YI
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,414B
FILING DATE: 20-JUNE-1998
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-100-414B-100

Query Match 47.1%; Score 64; DB 3; Length 42;
Best Local Similarity 64.7%; Pred. No. 0.0023;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 RYTHPHLPKDIVRSIAK 18
Db 25 RYTHPHLPRAIMRSTTK 41

RESULT 13
US-09-303-323-98
Sequence 98, Application US/09303323
Patent No. 6228987
GENERAL INFORMATION:
APPLICANT: Wang, Chang YI
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,323

```

: FILING DATE: 30-APR-1999
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/100,414
: FILING DATE: 20-JUNE-1998
: ATTORNEY/AGENT INFORMATION:
: NAME: Maria H. Lin
: REGISTRATION NUMBER: 29,323
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212-751-6849
: TELEFAX: 212-751-6849
: INFORMATION FOR SEQ ID NO: 98:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 42 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-09-303-323-98

Query Match          47.1%; Score 64; DB 4; Length 42;
Best Local Similarity 64.7%; Pred. No. 0.0023;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      2 RVTHPHLPKDIVRSIAK 18
        |||||||: ::|||
Db       25 RVTHPHLPALMRSTTK 41

RESULT 14
US-09-303-323-99
: Sequence 99, Application US/09303323
: Patent No. 6228987
: GENERAL INFORMATION:
: APPLICANT: Wang, Chang YI
: TITLE OF INVENTION: NOVEL LHRH PEPTIDE
: NUMBER OF SEQUENCES: 106
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Morgan & Flinnegan, L.L.P.
: STREET: 345 Park Avenue
: CITY: New York
: STATE: NY
: COUNTRY: USA
: ZIP: 10154-0054
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC Windows
: SOFTWARE: Word 97
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/303,323
: FILING DATE: 30-APR-1999
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/100,414
: FILING DATE: 20-JUNE-1998
: ATTORNEY/AGENT INFORMATION:
: NAME: Maria H. Lin
: REGISTRATION NUMBER: 29,323
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212-751-6849
: TELEFAX: 212-751-6849
: INFORMATION FOR SEQ ID NO: 99:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 42 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-09-303-323-99
```

Query Match 47.1%; Score 64; DB 4; Length 42;
Best Local Similarity 64.7%; Pred. No. 0.0023;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 RVTHPHLPKDIVRSIAK 18
 |||||||: ::|||
Db 25 RVTHPHLPALMRSTTK 41

```

RESULT 15
US-09-303-323-100
: Sequence 100, Application US/09303323
: Patent No. 6228987
: GENERAL INFORMATION:
: APPLICANT: Wang, Chang YI
: TITLE OF INVENTION: NOVEL LHRH PEPTIDE
: NUMBER OF SEQUENCES: 106
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Morgan & Flinnegan, L.L.P.
: STREET: 345 Park Avenue
: CITY: New York
: STATE: NY
: COUNTRY: USA
: ZIP: 10154-0054
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC Windows
: SOFTWARE: Word 97
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/303,323
: FILING DATE: 30-APR-1999
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/100,414
: FILING DATE: 20-JUNE-1998
: ATTORNEY/AGENT INFORMATION:
: NAME: Maria H. Lin
: REGISTRATION NUMBER: 29,323
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212-751-6849
: TELEFAX: 212-751-6849
: INFORMATION FOR SEQ ID NO: 100:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 42 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-09-303-323-100
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Query Match 47.1%; Score 64; DB 4; Length 42;
Best Local Similarity 64.7%; Pred. No. 0.0023;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 RVTHPHLPKDIVRSIAK 18
 |||||||: ::|||
Db 25 RVTHPHLPALMRSTTK 41

Search completed: July 15, 2002, 12:45:40
Job time: 21 sec

GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: 19F Antagonists
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,539D
FILING DATE: 21-Apr-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/178583
FILING DATE: 07-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/744768
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P0718P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-232-539D-56

Query Match 57.4%; Score 78; DB 2; Length 113;
Best Local Similarity 61.9%; Pred. No. 4.7e-05;
Matches 13; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 CRVTHPHLPKDIVSIKAPG 21
|||||||:|:| | |
Db 91 CRVTHPHLPALMRSTTKTSG 111

RESULT 6
US-08-466-151-1
Sequence 1, Application US/08466151
Patent No. 6037453
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/466,151
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/466163
FILING DATE: 06-Jun-1995
APPLICATION NUMBER: 08/405617
FILING DATE: 15-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/185899
FILING DATE: 26-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/879495
FILING DATE: 07-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/744768
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P0718P2C1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
US-08-466-151-1

Query Match 49.6%; Score 67.5; DB 3; Length 118;
Best Local Similarity 59.1%; Pred. No. 0.0022;
Matches 13; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 1 CRVTHPHLPKDI-VRSIAKAPG 21
|||||||:|:| | |
Db 96 CRVTHPHLPALMRSTTKTSG 117

RESULT 7
US-08-464-025A-1
Sequence 1, Application US/08464025A
Patent No. 5994514
GENERAL INFORMATION:
APPLICANT: Jardieu et al.
TITLE OF INVENTION: IMMUNOGLOBULIN VARIANTS
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,025A
FILING DATE: 05-Jun-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P0718C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-464-025A-1

Query Match 49.6%; Score 67.5; DB 2; Length 119;
Best Local Similarity 59.1%; Pred. No. 0.0022;
Matches 13; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 1 CRVTHPLPKDIVRSIAK 21
|||||||:|:|:|:|
DB 97 CRVTHPLPKALMRSTK 118

RESULT 8
US-09-100-414B-95
; Sequence 95, Application US/09100414B
; Patent No. 6025468
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Y1
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Flinnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,414B
; FILING DATE: 20-JUNE-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-751-6849
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-100-414B-95

Query Match 47.1%; Score 64; DB 3; Length 25;
Best Local Similarity 64.7%; Pred. No. 0.0012;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 RVTTHPLPKDIVRSIAK 18
|||||||:|:|:|:|
DB 8 RVTTHPLPKALMRSTK 24

RESULT 9
US-09-303-323-95
; Sequence 95, Application US/09303323
; Patent No. 6228987
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Y1
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE

TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Flinnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,323
FILING DATE: 30-APR-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-751-6849
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-303-323-95

Query Match 47.1%; Score 64; DB 4; Length 25;
Best Local Similarity 64.7%; Pred. No. 0.0012;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 RVTTHPLPKDIVRSIAK 18
|||||||:|:|:|:|
DB 8 RVTTHPLPKALMRSTK 24

RESULT 10
US-09-100-414B-98
; Sequence 98, Application US/09100414B
; Patent No. 6025468
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Y1
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Flinnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,414B
; FILING DATE: 20-JUNE-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 15, 2002, 12:45:19 ; Search time 15.25 Seconds
(without alignments)
157.523 Million cell updates/sec

Title: US-09-938-700-4
Perfect score: 136
Sequence: 1 CRVTHPLPKDIVRSIAKAPGKRAP 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | DB ID | Description |
|------------|-------|--------------------|---------------|--------------------|
| 1 | 105 | 77.2 | 429 1 EHRT | Ig epsilon chain C |
| 2 | 89 | 65.4 | 426 2 I36948 | Ig epsilon chain C |
| 3 | 86 | 63.2 | 428 1 EHHU | Ig epsilon chain C |
| 4 | 80 | 58.8 | 388 1 EHHM | Ig epsilon chain C |
| 5 | 80 | 58.8 | 548 2 S38864 | Ig epsilon chain C |
| 6 | 67 | 49.3 | 107 2 I68730 | IgE chain C3 regio |
| 7 | 67 | 49.3 | 107 2 I68726 | IgE chain C3 regio |
| 8 | 59 | 43.4 | 684 2 S60266 | novel antigen rece |
| 9 | 58 | 42.6 | 549 2 S04845 | Ig heavy chain pre |
| 10 | 54 | 39.7 | 1938 1 S06005 | myosin alpha heavy |
| 11 | 54 | 39.7 | 1939 1 A46762 | myosin alpha heavy |
| 12 | 54 | 39.7 | 1939 2 I48175 | myosin heavy chain |
| 13 | 52 | 38.2 | 273 2 B87319 | hypothetical prote |
| 14 | 51 | 37.5 | 572 2 T35963 | Ig y heavy chain (|
| 15 | 51 | 37.5 | 572 2 B46529 | alpha cardiac myos |
| 16 | 51 | 37.5 | 1938 1 I49464 | myosin heavy chain |
| 17 | 51 | 37.5 | 1940 1 S04090 | myosin heavy chain |
| 18 | 51 | 37.5 | 1940 1 A24922 | myosin heavy chain |
| 19 | 50.5 | 37.1 | 277 2 I47162 | Ig gamma 4 chain C |
| 20 | 50.5 | 37.1 | 327 1 G4HU | Ig gamma 4 chain C |
| 21 | 50.5 | 37.1 | 328 2 I47161 | Ig gamma 3 chain C |
| 22 | 50.5 | 37.1 | 328 2 I47158 | Ig gamma 1 chain C |
| 23 | 50.5 | 37.1 | 328 2 I47160 | Ig gamma 2b chain |
| 24 | 50.5 | 37.1 | 328 2 I47159 | Ig gamma 2a chain |
| 25 | 50.5 | 37.1 | 330 1 G2MSA | Ig gamma-2a chain |
| 26 | 50.5 | 37.1 | 399 1 G2MSAM | Ig gamma-2a chain |
| 27 | 50.5 | 37.1 | 446 2 S40295 | Ig gamma-2a chain |
| 28 | 50.5 | 37.1 | 469 2 S37483 | Ig gamma-2a chain |
| 29 | 50.5 | 37.1 | 538 2 A83972 | hypothetical prote |

| | | | | |
|----|------|------|---------------|--------------------|
| 30 | 50 | 36.8 | 1038 1 MWRBCB | myosin beta heavy |
| 31 | 50 | 36.8 | 1934 2 I48153 | myosin beta heavy |
| 32 | 50 | 36.8 | 1935 1 A37102 | myosin beta heavy |
| 33 | 50 | 36.8 | 1935 1 S06006 | myosin heavy chain |
| 34 | 50 | 36.8 | 1935 2 A59286 | myosin heavy chain |
| 35 | 49.5 | 36.4 | 405 1 G2MSM | Ig gamma-2b chain |
| 36 | 49.5 | 36.4 | 474 1 G2MSI1 | Ig gamma-2b chain |
| 37 | 49.5 | 36.4 | 573 2 S12838 | Ig mu chain precu |
| 38 | 49 | 36.0 | 1937 2 I38055 | myosin heavy chain |
| 39 | 49 | 36.0 | 1938 1 JX0178 | myosin heavy chain |
| 40 | 48.5 | 35.7 | 166 2 C72641 | hypothetical prote |
| 41 | 48.5 | 35.7 | 234 2 PT0207 | Ig gamma chain C r |
| 42 | 48.5 | 35.7 | 255 4 S31866 | Ig gamma-1 chain C |
| 43 | 48.5 | 35.7 | 329 2 S00847 | Ig gamma-2c chain |
| 44 | 48.5 | 35.7 | 330 1 GHHU | Ig gamma-1 chain C |
| 45 | 48.5 | 35.7 | 374 2 S69339 | Ig heavy chain V r |

ALIGNMENTS

RESULT 1

EHRT Ig epsilon chain C region - rat

C:Species: Rattus norvegicus (Norway rat)
C:Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 16-Jul-1999

C:Accession: A93442; A90937; A02143
C:Accession: A93442; A90937; A02143

R:Hellman, L.; Pettegerson, U.; Engstrom, A.; Karlsson, T.; Bennich, H.
Nucleic Acids Res. 10, 6041-6049, 1982

A:Title: Structure and evolution of the heavy chain from rat immunoglobulin E.
A:Reference number: A93442; MUID:83064537

A:Accession: A93442
A:Molecule type: mRNA

A:Residues: 1-429 <HELD>
A:Experimental source: strain LOU/C/MSL, immunocytoma IR2

R:Kinsvogel, W.R.; Reddy, E.P.; Moore, J.M.; Faust Jr., C.H.
DNA 1, 335-343, 1982

A:Title: A cloned cDNA probe for rat immunoglobulin epsilon heavy chain: construction
A:Reference number: A90937; MUID:83182019

A:Accession: A90937
A:Contents: myeloma IRL62

A:Molecule type: mRNA
A:Residues: 'N', 169-307, 'Y', 309-342 <KIN>

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into

C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F:19-80/Domain: immunoglobulin homology <IM1>
F:118-186/Domain: immunoglobulin homology <IM2>

F:223-291/Domain: immunoglobulin homology <IM3>
F:327-398/Domain: immunoglobulin homology <IM4>

F:46,99,170,240,265,369,419/Binding site: carbohydrate (Asn) (covalent) #status predi

Query Match 77.2%; Score 105; DB 1; Length 429;

Best Local Similarity 79.2%; Pred. No. 2.4e-07;
Matches 19; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CRVTHPLPKDIVRSIAKAPGKRRA 24

DB 289 CRVTHPLPKDIVRSIAKAPGKRRA 312

RESULT 2
I36948 Ig epsilon chain - chimpanzee (fragment)

C:Species: Pan troglodytes (chimpanzee)
C:Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 21-Jan-2000

C:Accession: I36948
R:Sakoyama, Y.; Hono, K.

Proc. Natl. Acad. Sci. U.S.A. 84, 1080-1084, 1987

A:Title: Nucleotide sequences of immunoglobulin epsilon genes of chimpanzee and orang

A:Accession: 136948
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-426 <RES>
 A:Cross-references: GB:M5398; NID:g176797; PIDN:AAA3416.1; PID:g176798
 C:Genetics:
 A:introns: 103/1; 209/1; 317/1
 C:Superfamily: Immunoglobulin C region; Immunoglobulin homology
 F:336-405/Domain: Immunoglobulin homology <IMM>

Query Match 65.48; Score 89; DB 2; Length 426;
 Best Local Similarity 66.7%; Pred. No. 4.8e-05;
 Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 Oy 1 CRYTHPLPKDIVRSIAKAGKRA 24
 Db 297 CRYTHPLPLALVSTTKISGPRNA 320

RESULT 3

EMBL

IG epsilon chain C region - human
 C:Species: Homo sapiens (man)

C:Date: 31-Mar-1981 #sequence revision 13-Jun-1983 #text change 16-Jul-1999

C:Accession: A22771; A23195; PH1214; A93491; A90824; A94418; B93933; S02438; A53116; C46

R:Flanagan, J.G.; Rabbits, T.H.

EMBO J. 1, 655-660, 1982

A:Title: The sequence of a human immunoglobulin epsilon heavy chain constant region gene

A:Reference number: A22771; MUID:84236029

A:Accession: A22771

A:Molecule type: DNA

A:Residues: 1-428 <FLA>

A:Cross-references: GB:I00022; GB:J00227; GB:V00555; NID:g185035

R:Ueda, S.; Nakai, S.; Nishida, Y.; Hasejima, H.; Honjo, T.

EMBO J. 1, 1539-1544, 1982

A:Title: Long terminal repeat-like elements flank a human immunoglobulin epsilon pseudog

A:Reference number: A23195; MUID:04207910

A:Accession: A23195

A:Molecule type: DNA

A:Residues: 2-428 <ED>

A:Cross-references: GB:J00222; NID:g184755

R:Zhang, K.; Saxon, A.; Max, E.E.

J. Exp. Med. 176, 233-243, 1992

A:Title: Two unusual forms of human immunoglobulin E encoded by alternative RNA splicing

A:Reference number: PH1214; MUID:92308839

A:Accession: PH1214

A:Molecule type: DNA

A:Residues: 320-428 <ZHA>

A:Cross-references: EMBL:X63693; GB:S38668; NID:g32987

Nucleic Acids Res. 11, 719-726, 1983

A:Title: Molecular cloning and nucleotide sequencing of human immunoglobulin epsilon cha

A:Reference number: A93491; MUID:83168897

A:Accession: A93491

A:Molecule type: mRNA

A:Residues: 1-428 <SEN>

A:Cross-references: GB:I00022; GB:J00227; GB:V00555; NID:g185035

R:Max, E.E.; Bailey, J.; Mey, R.; Kirsch, I.R.; Leder, P.

Cell 29, 691-699, 1982

A:Title: Duplication and deletion in the human immunoglobulin epsilon genes.

A:Reference number: A90824; MUID:83001945

A:Accession: A90824

A:Molecule type: DNA

A:Residues: 1-358, 1-360-428 <MAX>

A:Cross-references: GB:J00222; NID:g184755

A:Note: This sequence difference may be due to polymorphism

in immediate hyperresponsivity: Modern Concepts and Developments, Bach, M.K., ed., pp. 1-3

A:Reference number: A94418

A:Accession: A94418

A:Molecule type: protein

A:Residues: 1-6, 1-8-16, 1-18-43, 1-45-52, 55-92, 95-97, 1-99-121, 1-123, 1-124

A:Experimental source: myeloma protein ND
 R:Kenten, J.H.; Molgaard, H.V.; Houghton, M.; Derbyshire, R.B.; Viney, J.; Bell, L.O.
 Proc. Natl. Acad. Sci. U.S.A. 79, 6661-6665, 1982

A:Title: Cloning and sequence determination of the gene for the human immunoglobulin

A:Reference number: A93933; MUID:83065234

A:Accession: B93933

A:Molecule type: mRNA

A:Residues: 1-40, 68-114, 427-428 <KEN>

A:Cross-references: GB:I00022; NID:g185035

R:Ikeyama, S.

FEBS Lett. 224, 306-310, 1987

A:Title: Purification and characterization of a recombinant human IgE Fc-epsilon frag

A:Reference number: S02438; MUID:88083534

A:Accession: S02438

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 98-352 <IKE>

R:Zhang, K.; Max, E.E.; Cheah, H.K.; Saxon, A.

J. Biol. Chem. 269, 456-462, 1994

A:Title: Complex alternative RNA splicing of epsilon-immunoglobulin transcripts produ

A:Reference number: A53116; MUID:94103254

A:Accession: A53116

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 320-428 <ZHA>

A:Experimental source: myeloma U266-derived cell line AF-10

A:Note: sequence extracted from NCBI backbone (NCBIN:141701, NCBI:141702)

Eur. J. Immunol. 23, 159-167, 1993

A:Title: Characterization of four novel epsilon chain mRNA and a comparative analysis

A:Reference number: A46536; MUID:93122085

A:Accession: C46536

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 382-426 <HEB>

A:Cross-references: GB:S55273; NID:g263166; PIDN:AA24857.1; PID:g263167

A:Experimental source: B cell myeloma U-266

A:Note: sequence extracted from NCBI backbone (NCBI:125297)

A:Accession: D46536

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 382-391 <HE2>

A:Cross-references: GB:S55276; NID:g263168; PIDN:AA24858.1; PID:g263169

A:Experimental source: B cell myeloma U-266

A:Note: sequence extracted from NCBI backbone (NCBI:125299)

A:Accession: A46536

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 401-428 <HE3>

A:Cross-references: GB:S53497; NID:g263162; PIDN:AA24855.1; PID:g263163

A:Experimental source: B cell myeloma U-266

A:Note: sequence extracted from NCBI backbone (NCBI:123483)

C:Genetics:

A:Gene: GDB:IGHE

A:Cross-references: GDB:119335; OMIM:147180

A:Map position: 14q32.33-14q32.33

A:introns: 1/1; 104/1; 211/1; 319/1

C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (

C:Superfamily: immunoglobulin C region; Immunoglobulin homology <IM3>

C:Keywords: alternative splicing; duplication; glycoprotein; heterotrimer; immunogl

F:128-195/Domain: Immunoglobulin homology <IM2>

F:232-301/Domain: Immunoglobulin homology <IM2>

F:338-407/Domain: Immunoglobulin homology <IM3>

F:14/Disulfide bonds: interchain (to light chain) #status predicted

F:15-105, 29-85, 135-193, 239-299, 345-405/Disulfide bonds: #status predicted

F:21, 49, 99, 146, 252, 275/Binding site: carbohydrate (Asn) (covalent) #status experiment

F:121, 209/Disulfide bonds: interchain (to heavy chain) #status predicted

Query Match 63.28; Score 86; DB 1; Length 428;
 Best Local Similarity 62.5%; Pred. No. 0.00013;

Matches 15; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 1 CRYTHPHLPKDIVRSIAKAPGKRA 24
 ||||| :||| :|||
 DB 299 CRYTHPHLPALMRSTKTSKCPRA 322

RESULT 4

EHMS

Ig epsilon chain C region (version 1) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 16-Jul-1999

C:Accession: A02144

R:Lin, F.T.; Albrandt, K.; Sutcliffe, J.G.; Katz, D.H.

Proc. Natl. Acad. Sci. U.S.A. 79, 7852-7856, 1982

A:Title: Cloning and nucleotide sequence of mouse immunoglobulin epsilon chain cDNA.

A:Reference number: A02144; MUID:83117774

A:Accession: A02144

A:Molecule type: mRNA

A:Residues: 1-388 <LTU>

A:Cross-references: GB:J00476; NID:q194875; PIDN:AAA38085.1; PID:q387220

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a

C:Superfamily: immunoglobulin C region: immunoglobulin homology

C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F:1-44/Domain: immunoglobulin homology <IM2>

F:81-149/Domain: immunoglobulin homology <IM3>

F:186-254/Domain: immunoglobulin homology <IM3>

F:290-361/Domain: immunoglobulin homology <IM4>

F:10,51,62,133,205,228,332,382/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 58.8%; Score 80; DB 1; Length 388;
 Best Local Similarity 62.5%; Pred. No. 0.00088;

Matches 15; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

OY 1 CRYTHPHLPKDIVRSIAKAPGKRA 24
 ||||| :||| :|||
 DB 252 CVDHDPFKPIVRSITKTPGQS 275

RESULT 5

Ig epsilon chain C region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-May-2001

C:Accession: S38864

R:Klapp, B.; Becker, W.; Schlaak, M.

submitted to the EMBL data library, November 1993

A:Description: Combination of a defined specificity and desired isotype by cloning of an

A:Reference number: S38864

A:Accession: S38864

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-548 <KIP>

A:Cross-references: EMBL:Z27397; NID:q416537; PIDN:CAA81768.1; PID:q940782

C:Superfamily: immunoglobulin C region: immunoglobulin homology

F:335-421/Domain: immunoglobulin homology <IMX>

Query Match 58.8%; Score 80; DB 2; Length 548;
 Best Local Similarity 62.5%; Pred. No. 0.0012;

Matches 15; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

OY 1 CRYTHPHLPKDIVRSIAKAPGKRA 24
 ||||| :||| :|||
 DB 419 CVDHDPFKPIVRSITKTPGQS 442

RESULT 6

Ig epsilon chain C3 region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-May-2001

C:Accession: S38864

R:Klapp, B.; Becker, W.; Schlaak, M.

submitted to the EMBL data library, November 1993

A:Description: Combination of a defined specificity and desired isotype by cloning of an

A:Reference number: S38864

A:Accession: S38864

A:Status: preliminary

A:Molecule type: mRNA

C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jan-2000

C:Accession: I68730

R:Shinkai, Y.; Nakachi, H.; Honjo, T.; Okumura, K.

Immunogenetics 27, 288-292, 1988

A:Title: Mouse immunoglobulin allotypes: Multiple differences between the nucleic acid

A:Reference number: I54443; MUID:88152907

A:Accession: I68730

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-107 <RES>

A:Cross-references: GB:I62933; NID:q194464; PIDN:AAA37915.1; PID:q194469

C:Superfamily: immunoglobulin C region: immunoglobulin homology

F:22-90/Domain: immunoglobulin homology <IMX>

Query Match 49.3%; Score 67; DB 2; Length 107;
 Best Local Similarity 65.0%; Pred. No. 0.018;

Matches 13; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CRYTHPHLPKDIVRSIAKAP 20
 ||||| :||| :|||
 DB 88 CVDHDPFKPIVRSITKTP 107

RESULT 7

Ig epsilon chain C3 region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jan-2000

C:Accession: I68726

R:Shinkai, Y.; Nakachi, H.; Honjo, T.; Okumura, K.

Immunogenetics 27, 288-292, 1988

A:Title: Mouse immunoglobulin allotypes: Multiple differences between the nucleic acid

A:Reference number: I54443; MUID:88152907

A:Accession: I68726

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-107 <RES>

A:Cross-references: GB:M22930; NID:q194455; PIDN:AAA37911.1; PID:q194460

C:Superfamily: immunoglobulin C region: immunoglobulin homology

F:22-90/Domain: immunoglobulin homology <IMX>

Query Match 49.3%; Score 67; DB 2; Length 107;
 Best Local Similarity 65.0%; Pred. No. 0.018;

Matches 13; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CRYTHPHLPKDIVRSIAKAP 20
 ||||| :||| :|||
 DB 88 CVDHDPFKPIVRSITKTP 107

RESULT 8

novel antigen receptor precursor - nurse shark

C:Species: Ginglymostoma cirratum (nurse shark)

C:Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 21-Jul-2000

C:Accession: S60266

R:Greenberg, A.S.; Avila, D.; Hughes, M.; McKimney, E.C.; Flajnik, M.F.

Nature 374, 168-173, 1995

A:Title: A new antigen receptor gene family that undergoes rearrangement and extensive

A:Reference number: S60266; MUID:95183140

A:Accession: S60266

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-684 <GRE>

A:Cross-references: EMBL:U18701; NID:q699442; PIDN:AAA8195.1; PID:q699443

Query Match 43.4%; Score 59; DB 2; Length 684;
 Best Local Similarity 50.0%; Pred. No. 1.7;

Matches 11; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 1 CRVTHPLPKDIVRSIAKAPG 22
Db 645 CLVGHPSLRDLIRSTKSNKG 666

RESULT 9

S04845
Ig heavy chain precursor - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 26-Aug-1999
C:Accession: S04845; S05695
R:Amemiya, C.T.; Haire, R.N.; Litman, G.W.
Nucleic Acids Res. 17, 5388, 1989
A:Title: Nucleotide sequence of a cDNA encoding a third distinct Xenopus immunoglobulin
A:Reference number: S04845; MUID:89345103
A:Accession: S04845
A:Molecule type: mRNA
A:Residues: 1-549 <AME>
A:Cross-references: EMBL:X15114
R:Litman, G.W.
Submitted to the EMBL Data Library, April 1989
A:Reference number: S05695
A:Accession: S05695
A:Molecule type: mRNA
A:Residues: 1-308 'H', 310-549 <LIT>
A:Cross-references: EMBL:X15114; NID:964799; PID:g763031
C:Superfamily: Immunoglobulin C region; Immunoglobulin homology
C:Keywords: glycoprotein; heterotrimer; immunoglobulin
F:26-109/Domain: Immunoglobulin homology <IMM>
F:281,294/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 42.6%; Score 58; DB 2; Length 549;
Best Local Similarity 52.2%; Pred. No. 1.9;
Matches 12; Conservative 3; Mismatches 6; Indels 2; Gaps 1;
OY 1 CRVTHPLPKDIVRSIAKAPG 21
Db 424 CRVHDPSPLEKSIQKSDPG 446

RESULT 10

S06005
myosin alpha heavy chain, cardiac muscle [similarity] - rat
N:Alternate names: alpha-myosin heavy chain
N:Contains: myosin ATPase (EC 3.6.1.32)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001
C:Accession: S06005; S07535; A20971; A02988; I53305
R:McNally, E.M.; Gianola, K.W.; Leinwand, L.A.
Nucleic Acids Res. 17, 7527-7528, 1989
A:Title: Complete nucleotide sequence of full length cDNA for rat alpha cardiac myosin
A:Reference number: S06005; MUID:90016822
A:Accession: S06005
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-1938 <MCN>
A:Cross-references: EMBL:X15938; NID:956654; PID:CAA3064.1; PID:g56655
R:McNally, E.M.; Kraft, R.; Bravo-Zehnder, M.; Taylor, D.A.; Leinwand, L.A.
J. Mol. Biol. 210, 665-671, 1989
A:Title: Full-length rat alpha and beta cardiac myosin heavy chain sequences. Comparison
A:Reference number: S07535; MUID:90133919
A:Accession: S07535
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1938 <MC2>
R:Mandavi, V.; Chambers, A.P.; Nadal-Ginard, B.
Proc. Natl. Acad. Sci. U.S.A. 81, 2626-2630, 1984
A:Title: Cardiac alpha- and beta-myosin heavy chain genes are organized in tandem.
A:Accession: A20971; MUID:84194059
A:Molecule type: protein
A:Residues: 1-12, 'AP', 14-45, 'A', 47-50, 'AP', 53-81, 'E', 83-86, 'Q', 88-109, 111-133, 'H', 135-16

R:Mandavi, V.; Periasamy, M.; Nadal-Ginard, B.
Nature 297, 659-664, 1982

A:Title: Molecular characterization of two myosin heavy chain genes expressed in the
A:Reference number: A02988; MUID:82220036
A:Accession: A02988
A:Molecule type: mRNA
A:Residues: 1512-1574 'S', 1576-1721, 'N', 1723-1851, 'N', 1853-1869, 'N', 1871-1933, 'T', 193
A:Note: there are 10 or more myosin heavy chain genes in the rat, at least two of whi
R:Mandavi, V.; Lompre, A.M.; Chambers, A.P.; Nadal-Ginard, B.
Eur. Heart J. 5, 181-191, 1984
A:Title: Cardiac myosin heavy chain isozymic transitions during development and under
A:Reference number: I53305; MUID:85179510
A:Accession: I53305
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1872-1933 'T', 1935-1938 <RES>
A:Cross-references: GB:I32697; NID:g205396; PID:AAA41658.1; PID:g205597
C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: actin binding; ATP; cardiac muscle; coiled coil; heart; hydrolase; methyl
F:87-767/Domain: myosin motor domain homology <MMOT>
F:177-184/Region: nucleotide-binding motif A (P-loop)
F:548-585/Region: actin binding #status predicted
F:656-678/Region: actin binding #status predicted
F:840-1938/Domain: coiled coil #status predicted <COI>
F:840-1280/Region: S2
F:1281-1938/Region: Light meromyosin
F:128/Modified site: N6,N6,N6-trimethyllysine (lys) #status predicted
F:183/Binding site: ATP (lys) #status predicted
F:696,706/Active site: Cys #status predicted

Query Match 39.7%; Score 54; DB 1; Length 1938;
Best Local Similarity 50.0%; Pred. No. 25;
Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
OY 2 RVTTHPLPKDIVRSIAKAPG 21
Db 664 RTTHPLPKDIVRSIAKAPG 683

RESULT 11

A46762
myosin alpha heavy chain, cardiac muscle - human
N:Contains: myosin ATPase (EC 3.6.1.32)
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001
C:Accession: A46762; A49354; S18830; B32562; B33835; B27858; A28908
R:Matsumoto, R.; Beisel, K.W.; Furutani, M.; Arai, S.; Takao, A.
Am. J. Med. Genet. 41, 537-547, 1991
A:Title: Complete sequence of human cardiac alpha-myosin heavy chain gene and amino a
A:Reference number: A46762; MUID:92133665
A:Accession: A46762
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-1939 <MAT>
A:Cross-references: DBJ:D00943; NID:g219523; PID:BA00791.1; PID:g219524
A:Accession: A46762
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1461 <MA2>
R:PPP, T.A.; Dixon, I.M.C.; Wang, H.Y.; Sole, M.J.; Llew, C.C.
Genomics 18, 505-509, 1993
A:Title: Structural organization of the human cardiac alpha-myosin heavy chain gene (
A:Reference number: A49354; MUID:4410346
A:Accession: A49354
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-87, 'Q', 89-573, 'Q', 575-607, 'A', 609-743, 'T', 745-789, 'W', 791-1013, 'V', 1015
-1039 <BPP>
A:Cross-references: GB:220656; NID:g297023; PID:CAA9695.1; PID:g297024
R:Brand, N.J.; Dabhadre, N.; Yacoub, M.; Barton, P.J.R.
Biochem. Biophys. Res. Commun. 179, 1255-1258, 1991
A:Title: Determination of the 5' exon structure of the human cardiac alpha-myosin hea

A:Reference number: S18830; MUID:9202859
 A:Accession: S18830
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-32

 A:Cross-references: EMBL:X56181; NID:928318; PIND:CAA39642.1; PID:928319
 R:Ramuchi-Takahara, K.; Sole, M.J.; Liew, J.; Ing, D.; Liew, C.C.
 Proc. Natl. Acad. Sci. U.S.A. 86, 3504-3508, 1989
 A:Title: Characterization of human cardiac myosin heavy chain genes.
 A:Reference number: A94224; MUID:89264452
 A:Accession: B32562
 A:Molecule type: DNA
 A:Residues: 1-87, 'Q', 89-177, 1551-1732, 'E', 1734-1736, 'T', 1738-1762, 'D', 1764-1848 <Y>
 R:Ramuchi-Takahara, K.; Sole, M.J.; Liew, J.; Ing, D.; Liew, C.C.
 Proc. Natl. Acad. Sci. U.S.A. 86, 7416-7417, 1989
 A:Reference number: A94226
 A:Accession: B33835
 A:Molecule type: DNA
 A:Residues: 1-87, 'Q', 89-177, 1551-1732, 'E', 1734-1736, 'T', 1738-1762, 'D', 1764-1939 <Y>
 R:Saiz, L.J.; Gianola, K.M.; McNally, E.M.; Peghail, R.; Eddy, R.; Shows, T.B.; Leinwand
 Nucleic Acids Res. 15, 5443-5459, 1987
 A:Title: Human cardiac myosin heavy chain genes and their linkage in the genome.
 A:Reference number: A93659; MUID:87260010
 A:Accession: B27858
 A:Molecule type: DNA
 A:Residues: 1-3, 'S', 5-10, 'T', 12, 14-67 <SAD>
 R:Kurabayashi, M.; Tsuchimoto, H.; Komuro, I.; Takaku, F.; Yazaki, Y.
 J. Clin. Invest. 82, 524-531, 1988
 A:Title: Molecular cloning and characterization of human cardiac alpha- and beta-form my
 human atrium.
 A:Reference number: A92770; MUID:88299163
 A:Accession: A28908
 A:Molecule type: mRNA
 A:Residues: 1407-1532, 'N', 1534-1539, 'W', 1541-1576, 'W', 1579-1704, 'E', 1707-1762, 'D', 1764
 A:Cross-references: GB:M21664; NID:9189006; PIND:AAA36344.1; PID:9386972
 A:Experimental source: fetal heart
 C:Genetics:
 A:Gene: GDB:MYH6
 A:Cross-references: GDB:120214; OMIM:160710
 A:Map position: 14q11.2-14q13
 C:Superfamily: myosin heavy chain; myosin motor domain homology
 C:Keywords: actin binding; ATP; cardiac muscle; coiled coil; heart; hydrolase; methylate
 F:88-768/Domain: myosin motor domain homology <CMOT>
 F:118-185/Region: nucleotide-binding motif A (P-loop)
 F:549-586/Region: actin binding #status predicted
 F:657-679/Region: actin binding #status predicted
 F:841-1939/Domain: coiled coil #status predicted <COI>
 F:841-1281/Region: S2
 F:1282-1939/Region: light meromyosin
 F:129/Modified site: N6,N6,N6-trimethyllysine (Lys) #status predicted
 F:164/Binding site: ATP (Lys) #status predicted
 F:697/Active site: Cys #status predicted

Query Match 39.7%; Score 54; DB 1; Length 1939;
 Best Local Similarity 50.0%; Pred. No. 25;
 Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
 QY 2 RYTHPHLPKDIYRSIAKAPG 21
 Db 665 RTTHPHFVRCILPNERKAPG 684

RESULT 12
 148175
 myosin heavy chain alpha, cardiac muscle [similarity] - golden hamster
 C:Species: Mesocricetus auratus (golden hamster)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 02-Feb-2001
 C:Accession: 148175; A23938
 R:Wang, R.; Sole, M.J.; Cukerman, E.; Liew, C.C.
 J. Mol. Cell. Cardiol. 26, 1155-1165, 1994
 A:Title: Characterization and nucleotide sequence of the cardiac alpha-myosin heavy chain

A:Reference number: 148153; MUID:95115033
 A:Accession: 148175
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1939 <RES>
 A:Cross-references: GB:U15351; NID:9402373; PIND:AA859701.1; PID:9402374
 R:Liew, C.C.; Jandreski, M.A.
 Proc. Natl. Acad. Sci. U.S.A. 83, 3175-3179, 1986
 A:Title: Construction and characterization of the alpha-form of a cardiac myosin heav
 A:Reference number: A23938; MUID:86205859
 A:Accession: A23938
 A:Molecule type: mRNA
 A:Residues: 1630-1843, 'R', 1845-1878, 'T', 1880-1927, 'N', 1929-1932, 1934-1939 <LIE>
 C:Genetics:
 A:Insertions: 67/3; 115/3; 168/1; 177/2; 214/3; 245/3; 267/1; 300/1; 334/3; 381/1; 470/3
 392/2; 1453/3; 1509/1; 1550/3; 1653/3; 1721/3; 1763/3; 1855/3; 1887/3; 1932/3
 C:Superfamily: myosin heavy chain; myosin motor domain homology
 C:Keywords: ATP; cardiac muscle; heart; nucleotide binding; P-loop
 F:88-768/Domain: myosin motor domain homology <CMOT>
 F:178-185/Region: nucleotide-binding motif A (P-loop)

Query Match 39.7%; Score 54; DB 2; Length 1939;
 Best Local Similarity 50.0%; Pred. No. 25;
 Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
 QY 2 RYTHPHLPKDIYRSIAKAPG 21
 Db 665 RTTHPHFVRCILPNERKAPG 684

RESULT 13
 B87319
 hypothetical protein CC0564 [imported] - Caulobacter crescentus
 C:Species: Caulobacter crescentus
 C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
 C:Accession: B87319
 R:Neuman, W.C.; Feldblum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg,
 B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko
 N.J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapito, L.; Venter, J.C.; Fraser, C
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A:Title: Complete Genome Sequence of Caulobacter crescentus.
 A:Reference number: A87249; MUID:21173698; PMID:11259647
 A:Accession: B87319
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-273 <STO>
 A:Cross-references: GB:AE005673; NID:913421756; PIND:AAK22550.1; GSPDB:GN00148
 C:Genetics:
 A:Gene: CC0564

Query Match 38.2%; Score 52; DB 2; Length 273;
 Best Local Similarity 40.6%; Pred. No. 6.8;
 Matches 13; Conservative 5; Mismatches 4; Indels 10; Gaps 2;
 QY 4 TRPHLP-KDIVS-----IAKAGKRAP 25
 Db 224 SRPHAPRNKDIIRSTIGKDKPLCARANGRRAP 255

RESULT 14
 T35963
 hypothetical protein SC9C7.12 - Streptomyces coelicolor
 C:Species: Streptomyces coelicolor
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C:Accession: T35963
 R:Seeger, K.J.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M
 submitted to the EMBL Data Library, January 1999
 A:Reference number: Z21551
 A:Accession: T35963
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA

| | | | | |
|-----------------------|--------|----------------|-------|---------------|
| Query Match | 37.5% | Score 51; | DB 2; | Length 197; |
| Best Local Similarity | 42.9%; | Pred. No. 6.8; | | |
| Matches | 9; | Conservative | 6; | Mismatches 6; |
| | | | | Indels 0; |
| | | | | Gaps 0; |

| | |
|--------|----|
| RESULT | 15 |
|--------|----|

Ig Y heavy chain (7.85) - duck
N:Alternate names: Ig gamma chain (7.85)
C:Species: Anas platyrhynchos (domestic duck)
C>Date: 18-Jun-1999 #sequence_revision 18-Nov-1994 #exl-change 21-Jul-2000
C:Accession: B46529; S20759
R:Magor, R.E.; Warr, G.W.; Middleton, D.; Wilson, M.R.; Higgins, D.A.
J:Jmolol 149, 3627-2633, 1992
A:Title: Structural relationship between the two Igy of the duck, Anas platyrhynchos: mc
A:Reference number: A46529; MUID:93017865
A:Accession: B46529
A:Status: preliminary
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-572 <MAC>
A:Cross-References: EMBL:X65219; NID:g62442; PIDN:CAA46322.1; PID:g62443
A:Experimental source: Spleen (NCBI backbone (NCBI:P116127)
A:Note: Sequence extracted from NCBI
C:Superfamily: Immunoglobulin C region; Immunoglobulin homology
C:Keywords: Immunoglobulin
E:37-120/Domain: Immunoglobulin homology <IM>

| | | | | |
|-----------------------|--------------|---------------|-------|-------------|
| Query Match | 37.5% | Score 51; | DB 2; | Length 572; |
| Best Local Similarity | 50.0% | Pred. No. 20; | | |
| Matches 11; | Conservative | | 9; | Indels 0; |
| | | | | Gaps 0; |

```
QY      1 CRVTHPLPKDIVRSIAKAPGK 22
         ||| | | : ||| | |
Db      442 CTYQHEDLPVPLGKSIAKHAGK 463
```

Search completed: July 15, 2002, 12:46:39
Job time: 80 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 15, 2002, 12:46:19 ; Search time 10.41 seconds
(without alignments)
92,986 Million cell updates/sec

Title: US-09-938-700-4

Sequence: 136
1 CRVTHPHLPKDIYRISAKAPGKRAP 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | DB ID | Description |
|------------|-------|-------|--------|-------|-------------|
| 1 | 105 | 77.2 | 429 | 1 | EPC_RAT |
| 2 | 86 | 63.2 | 428 | 1 | EPC_HUMAN |
| 3 | 80 | 58.8 | 421 | 1 | EPC_MOUSE |
| 4 | 54 | 42.1 | 1938 | 1 | MYH6_RAT |
| 5 | 54 | 39.7 | 1939 | 1 | MYH6_HUMAN |
| 6 | 54 | 39.7 | 1939 | 1 | MYH6_MESAU |
| 7 | 51 | 37.5 | 1938 | 1 | MYH6_MOUSE |
| 8 | 51 | 37.5 | 1940 | 1 | MYH3_HUMAN |
| 9 | 51 | 37.5 | 1940 | 1 | MYH3_RAT |
| 10 | 50.5 | 37.1 | 327 | 1 | GCA_HUMAN |
| 11 | 50.5 | 37.1 | 330 | 1 | GCA_MOUSE |
| 12 | 50.5 | 37.1 | 399 | 1 | MYH7_RABIT |
| 13 | 50 | 36.8 | 736 | 1 | MYH7_MESAU |
| 14 | 50 | 36.8 | 1934 | 1 | MYH7_HUMAN |
| 15 | 50 | 36.8 | 1935 | 1 | MYH7_MOUSE |
| 16 | 50 | 36.8 | 1935 | 1 | MYH7_PIG |
| 17 | 50 | 36.8 | 1935 | 1 | MYH7_RAT |
| 18 | 49.5 | 36.4 | 336 | 1 | GCB_MOUSE |
| 19 | 49.5 | 36.4 | 374 | 1 | SPOD_HUMAN |
| 20 | 49.5 | 36.4 | 405 | 1 | GCB_MOUSE |
| 21 | 49 | 36.0 | 1937 | 1 | MYH8_HUMAN |
| 22 | 49 | 36.0 | 1938 | 1 | MYH8_MOUSE |
| 23 | 49 | 36.0 | 1939 | 1 | MYH8_CHICK |
| 24 | 49 | 36.0 | 1939 | 1 | MYH8_HUMAN |
| 25 | 49 | 36.0 | 1941 | 1 | MYH8_MOUSE |
| 26 | 48.5 | 35.7 | 329 | 1 | GCC_RAT |
| 27 | 48.5 | 35.7 | 330 | 1 | GCC_HUMAN |
| 28 | 48 | 35.3 | 836 | 1 | Y167_HUMAN |
| 29 | 48 | 35.3 | 1935 | 1 | GCL_HUMAN |
| 30 | 47 | 34.6 | 368 | 1 | LNK_RAT |
| 31 | 47 | 34.6 | 384 | 1 | GBAI_LICES |
| 32 | 47 | 34.6 | 392 | 1 | CARS_RHINI |
| 33 | 47 | 34.6 | 416 | 1 | MKR2_HUMAN |

| | | | | | | |
|----|------|------|------|---|------------|---------------------|
| 34 | 47 | 34.6 | 548 | 1 | LNK_MOUSE | O09039 mus musculus |
| 35 | 47 | 34.6 | 1938 | 1 | MYH8_HUMAN | O90kx3 homo sapien |
| 36 | 47 | 34.6 | 1940 | 1 | MYH3_CHICK | P02565 gallus gall |
| 37 | 46.5 | 34.2 | 341 | 1 | GLK_RHLO | O96d82 rhizobium 1 |
| 38 | 46 | 33.8 | 329 | 1 | GC3_MOUSE | P22436 mus musculus |
| 39 | 46 | 33.8 | 391 | 1 | MUCB_HUMAN | P04220 homo sapien |
| 40 | 46 | 33.8 | 398 | 1 | GC3M_MOUSE | P03987 mus musculus |
| 41 | 46 | 33.8 | 454 | 1 | MUC_HUMAN | P01871 homo sapien |
| 42 | 46 | 33.8 | 605 | 1 | FETA_MOUSE | P02772 mus musculus |
| 43 | 45.5 | 33.5 | 647 | 1 | SOHC_RHIN | P55348 rhizobium s |
| 44 | 45 | 33.1 | 412 | 1 | DOK2_MOUSE | O70469 mus musculus |
| 45 | 44.5 | 32.7 | 281 | 1 | Y4RD_RHIN | P55637 rhizobium s |

ALIGNMENTS

| RESULT | ID | STANDARD | PRT | 429 AA. |
|--------|---|----------|-----|---------|
| 1 | EPC_RAT | | | |
| AC | P01855; | | | |
| DT | 21-JUL-1986 (Rel. 01, Created) | | | |
| DT | 21-JUL-1986 (Rel. 01, Last sequence update) | | | |
| DT | 15-JUL-1999 (Rel. 38, Last annotation update) | | | |
| DE | Ig epsilon chain C region. | | | |
| OS | Rattus norvegicus (Rat). | | | |
| OC | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. | | | |
| OX | NCBI_TaxID=10116; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. (IMMUNOCYTOMA IR2). | | | |
| RC | STRAIN=LOU/C/MSL; | | | |
| RX | MEDLINE=83064537; PubMed=6292865; | | | |
| RA | Hellman L., Petersson U., Engstrom A., Karlsson T., Bennich H.; | | | |
| RT | "Structure and evolution of the heavy chain from rat immunoglobulin E."; | | | |
| RL | Nucleic Acids Res. 10:6041-6049(1982). | | | |
| RN | [2] | | | |
| RP | SEQUENCE OF 168-342 FROM N.A. (MYELOMA IR162). | | | |
| RX | MEDLINE=83182019; PubMed=6820340; | | | |
| RA | Kindsvoel W.R., Reddy E.P., Moore J.M., Faust C.H. Jr.; | | | |
| RT | "A cloned cDNA probe for rat immunoglobulin epsilon heavy chain: construction, identification, and DNA sequence."; | | | |
| RL | DNA 1:335-343(1982). | | | |
| RN | [3] | | | |
| RP | SEQUENCE OF 205-306 FROM N.A. | | | |
| RX | MEDLINE=82174576; PubMed=6803238; | | | |
| RA | Hellman L., Petersson U., Bennich H.; | | | |
| RT | "Characterization and molecular cloning of the mRNA for the heavy (epsilon) chain of rat immunoglobulin E."; | | | |
| RL | Proc. Natl. Acad. Sci. U.S.A. 79:1264-1266(1982). | | | |
| CC | ----- | | | |
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| CC | ----- | | | |
| CC | EMBL: J00744; AAA41379.1; ALT_INIT. | | | |
| CC | PIR: A02143; EHRT. | | | |
| DR | HSSP: P01854; 11GE. | | | |
| DR | InterPro: IPR003006; Ig_MHC. | | | |
| DR | InterPro: IPR003597; Ig_C1. | | | |
| DR | InterPro: IPR003600; Ig_Like. | | | |
| DR | Pfam: PF00047; Ig_4. | | | |
| DR | SMART: SM00410; Ig_Like; 3. | | | |
| DR | SMART: SM00407; IG_C1; 1. | | | |
| DR | PROSITE: PS00290; IG_MHC; 3. | | | |
| KW | Immunoglobulin domain; Immunoglobulin C region. | | | |
| FT | NON_TER | | | |
| FT | CONFLICT | | | |
| FT | 168 | | | |
| FT | 168 | | | |
| FT | R -> N (IN REF. 2). | | | |

FT CONFLICT 308 308 P -> L (IN REF. 2).
 SQ SEQUENCE 429 AA; 48671 MW; D2970B34FE8A72B0 CRC64;
 Query Match 77.2%; Score 105; DB 1; Length 429;
 Best Local Similarity 79.2%; Pred. No. 7.5e-08;
 Matches 19; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 CRVTHPHLPKDIYRSIAKAPGKRA 24
 DB 289 CRVDHPHFPKPIVRSITKAPGKRS 312
 RESULT 2
 EPC_HUMAN STANDARD; PRT; 428 AA.
 AC P01854;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ig epsilon chain C region.
 GN IGHE.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN 111
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83168897; Pubmed=6300763;
 RA Seno M., Kurokawa T., Ono Y., Onda H., Sasada R., Igarashi K.,
 RA Kikuchi M., Sugino Y., Nishida Y., Honjo T.;
 RT "Molecular cloning and nucleotide sequencing of human immunoglobulin
 RT epsilon chain cDNA.";
 RL Nucleic Acids Res. 11:719-726(1983).
 RN 121
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83001945; Pubmed=6288268;
 RA Max E.E., Battey J., Ney R., Kirsch I.R., Leder P.;
 RT "Duplication and deletion in the human immunoglobulin epsilon genes";
 RL Cell 29:691-699(1982).
 RN 131
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84236029; Pubmed=6234164;
 RA Flanagan J.G., Rabbitts T.H.;
 RT "The sequence of a human immunoglobulin epsilon heavy chain constant
 RT region gene, and evidence for three non-allelic genes.";
 RL EMBO J. 1:655-660(1982).
 RN 141
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84207910; Pubmed=6327276;
 RA Ueda S., Nakai S., Nishida Y., Hisajima H., Honjo T.;
 RT "Long terminal repeat-like elements flank a human immunoglobulin
 RT epsilon pseudogene that lacks introns.";
 RL EMBO J. 1:1539-1544(1982).
 RN 151
 RP PRELIMINARY SEQUENCE (MYELOMA PROTEIN ND).
 RA Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
 RT (in) Bach M.K. (eds.);
 RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,
 RL Marcel Dekker, New York (1978).
 RN 161
 RP SEQUENCE OF 1-40; 68-114 AND 427-428 FROM N.A.
 RX MEDLINE=83065234; Pubmed=6815656;
 RA Kenen J.H., Wolgast H.V., Houghton M., Derbyshire R.B., Viney J.,
 RA Bell L.O., Gould H.J.;
 RT "Cloning and sequence determination of the gene for the human
 RT immunoglobulin epsilon chain expressed in a myeloma cell line";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
 RN 171
 RP 3D-STRUCTURE MODELING.
 RA Padyn E.A., Davies D.R.;
 RT "A model of the Fc-epsilon of immunoglobulin E";
 RL Submitted (JUL-1993) to the PDB data bank.

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 CC -----
 DR EMBL: L00022; AAB59424.1; ALT_INIT.
 DR PIR: A02142; EHHH.
 DR PIR: A22771; A22771.
 DR PIR: A23195; A23195.
 DR PDB: 1IGE; 15-JUL-92.
 DR MIM: 147180;
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003597; Ig_c1.
 DR Pfam: PF00047; Ig; 4
 DR SMART: SM00407; IGc1; 4.
 DR PROSITE: PS00290; IG_MHC; 3.
 KM Immunoglobulin domain; Immunoglobulin C region; glycoprotein;
 KK 3D-structure.
 FT NON-TER 1 1
 FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 15 105
 FT DISULFID 29 85 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 121 121 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 135 193 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 209 209 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 239 299
 FT DISULFID 345 405
 FT CARBOHYD 21 21 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 49 49 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 99 99 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 275 275 N-LINKED (GLCNAC. . .).
 FT VARIANT 359 359 W -> L (IN REF. 2, POSSIBLY DUE TO
 FT POLYMERIZATION).
 FT FTID=VAR-003885.
 FT SEQUENCE 428 AA; 47019 MW; 25C4CA072AA558A0 CRC64;
 FT SQ
 Query Match 63.2%; Score 86; DB 1; Length 428;
 Best Local Similarity 62.5%; Pred. No. 4.3e-05;
 Matches 15; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
 QY 1 CRVTHPHLPKDIYRSIAKAPGKRA 24
 DB 299 CRVTHPHLPKPIVRSITKAPGKRS 322
 RESULT 3
 EPC_MOUSE STANDARD; PRT; 421 AA.
 AC P06336; P01856;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig epsilon chain C region.
 GN Mus musculus (Mouse).
 OS Mus musculus; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN 111
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84236092; Pubmed=6329728;
 RA Ishida N., Ueda S., Hayashida H., Miyata T., Honjo T.;
 RT "The nucleotide sequence of the mouse immunoglobulin epsilon gene:
 RT comparison with the human epsilon gene sequence.";
 RL EMBO J. 1:1117-1123(1982).
 RN 121
 RP REVISIONS.

RA Honjo T.;
 RU Submitted (APR-1986) to the EMBL/GenBank/DBJ databases.
 RN [1]
 RP SEQUENCE OF 34-421 FROM N.A.
 RX MEDLINE=8311774; PubMed=6818553;
 RA Liu F.-T., Albrandt K., Sutcliffe J.G., Katz D.H.;
 RT "Cloning and nucleotide sequence of mouse immunoglobulin epsilon
 chain cDNA."
 RL Proc. Natl. Acad. Sci. U.S.A. 79:7852-7856(1982).
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 CC -----
 DR EMBL: X01857; CAA25977.1; -;
 DR EMBL: X01857; CAA25978.1; -;
 DR PIR: A02145; EHMS.
 DR PIR: A02144; EHMS.
 DR HSSP: P01854; 116E.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003597; Ig-cl.
 DR InterPro: IPR003600; Ig-like.
 DR Pfam: PF00047; Ig_4.
 DR SMART: SM00410; Ig_Like; 2.
 DR SMART: SM00407; IgC1; 2.
 DR PROSITE: PS00290; IG_MHC; 3.
 DR Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
 KW NON_TER
 FT DOMAIN 1 90 CH1.
 FT DOMAIN 91 197 CH2.
 FT DOMAIN 198 304 CH3.
 FT DOMAIN 305 421 CH4.
 FT DISULFID 23 75 BY SIMILARITY.
 FT DISULFID 121 180 BY SIMILARITY.
 FT DISULFID 226 285 BY SIMILARITY.
 FT DISULFID 330 392 BY SIMILARITY.
 FT CARBOHYD 43 43 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 365 365 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 415 415 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 421 AA: 47320 MW: 8F909E1F30A06B47 CRC64;

Query Match 58.8%; Score 80; DR 1; Length 421;
 Best Local Similarity 62.5%; Pred. No. 0.00011;
 Matches 15; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

OY 1 CRYTHPHLPKDIVRSIAKPGKRA 24
 DB 285 CYDHPDFKPIVRSITKTGQRS 308

RESULT 4
 MYH6_RAT
 ID MYH6_RAT
 AC P02563; 063351; STANDARD; PRT; 1938 AA.
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Myosin heavy chain, cardiac muscle alpha isoform (MyHC-alpha).
 GN MYH6.
 OS Rattus norvegicus (Rat).
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=90016822; PubMed=2798111;
 RA Krate R., Bravo-Zehnder M., Taylor D., Leinwand L.A.;
 RT "Complete nucleotide sequence of full length cDNA for rat alpha
 chain cardiac myosin heavy chain."
 RL Nucleic Acids Res. 17:7527-7528(1989).
 RN [2]
 RP DISCUSSION OF SEQUENCE. PubMed=2614840;
 RX MEDLINE=90133919; PubMed=2614840;
 RA McNally E.M., Kraft R., Bravo-Zehnder M., Taylor D., Leinwand L.A.;
 RT "Full-length rat alpha and beta cardiac myosin heavy chain sequences.
 Comparisons suggest a molecular basis for functional differences."
 J. Mol. Biol. 210:665-671(1989).
 RN [3]
 RP SEQUENCE OF 1-167 FROM N.A.
 RX MEDLINE=84194059; PubMed=6585819;
 RA Mahdavi V., Chambers A.P., Nadal-Ginard B.;
 RT "Cardiac alpha- and beta-myosin heavy chain genes are organized in
 tandem."
 RL Proc. Natl. Acad. Sci. U.S.A. 81:2626-2630(1984).
 RN [4]
 RP SEQUENCE OF 1512-1938 FROM N.A.
 RX MEDLINE=82220036; PubMed=7045682;
 RA Mahdavi V., Periasamy M., Nadal-Ginard B.;
 RT "Molecular characterization of two myosin heavy chain genes expressed
 in the adult heart."
 RL Nature 297:659-664(1982).
 RN [5]
 RP SEQUENCE OF 1872-1938 FROM N.A.
 RC STRAIN=MSTAR; TISSUE=Heart;
 RX MEDLINE=83179510; PubMed=6241892;
 RA Mahdavi V., Lompre A.M., Chambers A.P., Nadal-Ginard B.;
 RT "Cardiac myosin heavy chain isozymic transitions during development
 and under pathological conditions are regulated at the level of mRNA
 availability."
 RL Eur. Heart J. 5:181-191(1984).
 CC -1- FUNCTION: MUSCLE CONTRACTION.
 CC -1- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
 CC HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
 CC AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
 CC -1- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
 CC -1- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
 CC CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
 CC CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
 CC -1- PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY
 CC ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY
 CC -1- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
 CC MEROMYOSIN (LM) AND 1 HEAVY MEROMYOSIN (HM). IT CAN LATER BE
 CC SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
 CC SUBFRAGMENT (S2).
 CC -1- MISCELLANEOUS: THE CARDIAC ALPHA ISOFORM IS A 'FAST' ATPASE
 CC MYOSIN, WHILE THE BETA ISOFORM IS A 'SLOW' ATPASE.
 CC -1- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 IQ DOMAIN.
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 CC -----
 DR EMBL: X15938; CAA34064.1; -;
 DR EMBL: X01464; AAA41648.1; -;
 DR EMBL: J00751; AAA41653.1; -;
 DR EMBL: M32697; AAA41658.1; -;
 DR PIR: S06005; S06005.
 DR PIR: A02988; A02988.
 DR HSSP: P08799; 1IMD.

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RA MEDLINE=94140346; PubMed=8307559;
RX Exp T.A., Dixon I.M., Meng H.Y., Sole M.J., Llew C.-C.;
RT "Structural organization of the human cardiac alpha-myosin heavy
RT chain gene (M16).";
RL Genomics 18:505-509(1993).
RN [3]
RP SEQUENCE OF 1-177 AND 1551-1939 FROM N.A.
RA MEDLINE=89264452; PubMed=7726733;
RX Yamauchi-Takahara K., Sole M.J., Llew J., Ing D., Llew C.-C.;
RT "Characterization of human cardiac myosin heavy chain genes.";
RT Proc. Natl. Acad. Sci. U.S.A. 86:3504-3508(1989).
RN [4]
RP ERRATUM.
RA Yamauchi-Takahara K., Sole M.J., Llew J., Ing D., Llew C.-C.;
RA Proc. Natl. Acad. Sci. U.S.A. 86:7416-7417(1989).
RN [5]
RP SEQUENCE OF 1407-1939 FROM N.A.
RX MEDLINE=88299163; PubMed=39669919;
RT Kurabayashi M., Tsuchimochi H., Komuro I., Takaku F., Yazaki Y.;
RT "Molecular cloning and characterization of human cardiac alpha- and
RT beta-form myosin heavy chain complementary DNA clones. Regulation of
RT expression during development and pressure overload in human
RT atrium.";
RL J. Clin. Invest. 82:524-531(1988).
RT [1]
CC -1- FUNCTION: MUSCLE CONTRACTION.
CC -1- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
CC HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
CC AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
CC -1- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
CC -1- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
CC CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
CC CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
CC -1- PTM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY
CC ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.
CC -1- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
CC SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (SI) AND 1 ROD-SHAPED
CC SUBFRAGMENT (S2).
CC -1- MISCELLANEOUS: THE CARDIAC ALPHA ISOFORM IS A 'FAST' ATPASE
CC MYOSIN, WHILE THE BETA ISOFORM IS A 'SLOW' ATPASE.
CC -1- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 IO DOMAIN
CC -----
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CC -----
DR EMBL; D00943; BA000791.1; -
DR EMBL; Z20656; CA79675.1; -
DR EMBL; M25140; AAA60386.1; -
DR EMBL; M25162; AAA60386.1; JOINED.
DR EMBL; M25142; AAA60387.1; -
DR EMBL; M25141; AAA60387.1; JOINED.
DR EMBL; M21664; AAA36344.1; -
DR PIR; A46762; A46762.
DR PIR; A28908; A28908.
DR HSSP; P08799; IIMD.
DR MIM; 160710; -
DR InterPro; IPR000048; IQ.
DR InterPro; IPR004009; Myosin_N.
DR InterPro; IPR002928; Myosin_tail.
DR InterPro; IPR001609; myosin_head.
DR Pfam; PF00612; IQ_2.
DR Pfam; PF00063; myosin_head.1.
DR Pfam; PF02736; Myosin_N.1.
DR Pfam; PF01576; Myosin_tail.1.
DR PRINTS; PR00193; MYOSINHEAVY.
DR ProDom; PD000355; myosin_head.1.
DR SMART; SM00015; IQ; 1.

```


SO SEQUENCE 1939 AA; 223626 MW; DBC8297DFE83115A CRC64;

Query Match 39.7%; Score 54; DB 1; Length 1939;
Best Local Similarity 50.0%; Pred. No. 8.7;
Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

OY 2 RYTHPHLEKDIVRSIAKAPG 21
1 1111 : : : 1111
DB 665 RTYHPHFVCLIPNERKAPG 684

RESULT 7

MYH6_MOUSE STANDARD; PRT: 1938 AA.

ID MYH6_MOUSE Q02566; Q64258; Q64738;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Myosin heavy chain, cardiac muscle alpha isoform (MYHC-alpha).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_Taxid=10090;

RV [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BALE/C, A/J, C57BL/6J, AND DBA/2J;

RC MEDLINE=92250040; PubMed=1577481;

RA Quinn-Laguer B K., Kennedy J E., Beliel K W.;

RT "Characterization of the allelic differences in the mouse cardiac

alpha-myosin heavy chain coding sequence.;

RT Genomics 13:176-186(1992).

RL [2]

RP SEQUENCE OF 1-67 FROM N.A.

RC STRAIN=AKR;

RC MEDLINE=91225025; PubMed=2026617;

RA Gullick J., Subramaniam A., Neumann J., Robbins J.;

RT "Isolation and characterization of the mouse cardiac myosin heavy

chain genes.;

RL J. Biol. Chem. 266:9180-9185(1991).

CC -1- FUNCTION: MUSCLE CONTRACTION.

CC -1- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2

HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)

CC -1- AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

CC -1- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

CC -1- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING

CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,

CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

CC -1- PTM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY

ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

CC -1- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT

MEROMYOSIN (LM) AND 1 HEAVY MEROMYOSIN (HM). IT CAN LATER BE

SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED

SUBFRAGMENT (S2).

CC -1- MISCELLANEOUS: THE CARDIAC ALPHA ISOFORM IS A 'FAST' ATPASE

CC -1- SIMILARITY: THE BETA ISOFORM IS A 'SLOW' ATPASE

CC -1- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.

CC -1- SIMILARITY: CONTAINS 1 IQ DOMAIN.

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CC -----

CC EMBL: M76598; AAA37159.1; -

DR EMBL: M76599; AAA37160.1; -

DR EMBL: M76600; AAA37161.1; -

DR EMBL: M76601; AAA37162.1; -

DR EMBL: M62404; AAA37424.1; -

DR HSSP: P08799; IMD.

DR SWISS-2DPAGE: Q02566; MOUSE.

DR MGD: MGI:97255; Myhca.

DR InterPro: IPR000048; IQ.

DR InterPro: IPR004009; Myosin_N.

DR InterPro: IPR002928; Myosin_tail.

DR InterPro: IPR001609; myosin_head.

DR Pfam: PF00612; IQ; 2.

DR Pfam: PF00063; myosin_head; 1.

DR Pfam: PF02736; Myosin_N; 1.

DR Pfam: PF01576; Myosin_tail; 1.

DR PRINTS: PR00193; MYOSINHEAVY.

DR ProDom: PD000355; myosin_head; 1.

DR SMART: SM00015; IQ; 1.

DR SMART: SM00242; MYSC; 1.

DR PROSITE: PS50096; IQ; 1.

DR Myosin: Muscle protein; Coiled coil; Thick filament; Actin-binding;

KW ATP-binding; Methylation; Alkylation; Multigene family;

KW Calmodulin-binding; Polymorphism.

FT DOMAIN 1 782 MYOSIN HEAD-LIKE.

FT DOMAIN 783 812 IQ.

FT DOMAIN 842 1938 COILED COIL (POTENTIAL).

FT NP_BIND 178 185 ATP.

FT DOMAIN 657 679 ACTIN-BINDING.

FT DOMAIN 759 773 ACTIN-BINDING.

FT DOMAIN 816 833 CALMODULIN-BINDING (BY SIMILARITY).

FT MOD_RES 129 129 METHYLATION (TR1) (POTENTIAL).

FT MOD_RES 697 697 ALKYLATION (SH-1) (POTENTIAL).

FT MOD_RES 707 707 ALKYLATION (SH-2) (POTENTIAL).

FT VARIANT 194 194 Y -> D.

FT VARIANT 545 545 S -> A.

FT VARIANT 838 838 I -> S.

FT VARIANT 838 838 I -> S.

SO SEQUENCE 1938 AA; 223564 MW; EAD789ADA6818FB CRC64;

Query Match 37.5%; Score 51; DB 1; Length 1938;
Best Local Similarity 45.0%; Pred. No. 24;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 2 RYTHPHLEKDIVRSIAKAPG 21
1 1111 : : : 1111
DB 665 KTYHPHFVCLIPNERKAPG 684

RESULT 8

MYH3_HUMAN STANDARD; PRT: 1940 AA.

ID MYH3_HUMAN Q1055; Q15492;

DT 01-JUL-1988 (Rel. 11, Created)

DT 01-JUL-1988 (Rel. 11, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Myosin heavy chain, fast skeletal muscle, embryonic (muscle embryonic

DE myosin heavy chain) (SMHCE).

GN MYH3.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_Taxid=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC MEDLINE=89263803; PubMed=2726495;

RA Eller M.S., Steadman H.H., Sylvester J.E., Fertels S.H.,

RA Rubinstein N.A., Kelly A.M., Sarkar S.;

RT "Nucleotide sequence of full length human embryonic myosin heavy

chain cDNA.;

RL Nucleic Acids Res. 17:3591-3592(1989).

RL [2]

RP SEQUENCE OF 774-1940 FROM N.A.

RC MEDLINE=90033298; PubMed=2806546;

RA Eller M.S., Steadman H.H., Sylvester J.E., Fertels S.H., Wu Q.-L.,

RA Raychowdhury M.K., Rubinstein N.A., Kelly A.M., Sarkar S.;

RT "human embryonic myosin heavy chain cDNA. Interspecies sequence

RT comparison.;

DR InterPro: IPR004009; Myosin_N.
 DR InterPro: IPR002928; Myosin_tail.
 DR InterPro: IPR002017; Spectrin.
 DR InterPro: IPR01609; myosin_head.
 DR Pfam: PF00612; IQ: 2.
 DR Pfam: PF00063; myosin_head; 1.
 DR Pfam: PF02736; Myosin_N; 1.
 DR Pfam: PF01576; Myosin_tail; 1.
 DR PRINTS: PR00193; MYOSINHEAD.
 DR ProDom: PD000355; myosin_head; 1.
 DR SMART: SM00015; IQ; 1.
 DR SMART: SM00242; MYSC; 1.
 DR PROSITE: PS50096; IQ; 1.
 KW Myosin; muscle protein; Coiled coil; Thick filament; Actin-binding;
 KW Calmodulin-binding; ATP-binding; Methylation; Alkylation;
 KW Multigene family.
 FT DOMAIN 1 781 MYOSIN HEAD-LIKE.
 FT DOMAIN 782 811 IQ.
 FT DOMAIN 840 1933 COILED COIL (POTENTIAL).
 FT NP_BIND 179 186 ATP (POTENTIAL).
 FT DOMAIN 656 678 ACTIN-BINDING.
 FT DOMAIN 758 772 ACTIN-BINDING.
 FT MOD_RES 130 130 METHYLATION (TRI-) (POTENTIAL).
 FT MOD_RES 696 696 METHYLATION (SH-1).
 FT MOD_RES 706 706 ALKYLATION (SH-2).
 SQ SEQUENCE 1940 AA; 223857 MW; B5D546A596E5A696 CRC64;

Query Match 37.58; Score 51; DB 1; Length 1940;
 Best Local Similarity 45.08; Pred. No. 24;
 Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

OY 2 RYTHPLPKDIYRSTAKAPG 21
 DB 664 RTTHPEVRCIIPNETKTPG 683

RESULT 10
 ID GC4_HUMAN STANDARD: PRT; 327 AA.
 AC P01861;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ig gamma-4 chain C region.
 GN IGHG4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_Taxid=9606;
 RP SEQUENCE FROM N.A.
 RP MEDLINE=83157104; PubMed=6299662;
 RA Ellison J.W., Buxbaum J.N., Hood L.E.;
 RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
 RL DNA 111-18(1981).
 RN [2]
 RP SEQUENCE OF 1-30 AND 81-326.
 RP MEDLINE=70207560; PubMed=4192699;
 RA Plink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
 RT "Human immunoglobulin subclasses. Partial amino acid sequence of the
 RL Blochem. J 117:33-47(1970).
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 CC or send an email to license@sib-sib.ch).
 CC EMBL, K01316; AAB59394.1; ALT_INIT.

DR PIR: A02150; G4HU.
 DR HSSP: P01842; 7FAB.
 DR MIM: 147130; -.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003597; Ig_C1.
 DR InterPro: IPR003600; Ig_Like.
 DR Pfam: PF00047; Ig; 3.
 DR SMART: SM00410; Ig_Like; 1.
 DR SMART: SM00407; IgC1; 2.
 DR PROSITE: PS00290; Ig_MHC; 2.
 KW Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1 1
 FT DOMAIN 1 98 CH1.
 FT DOMAIN 99 110 HINGE.
 FT DOMAIN 111 220 CH2.
 FT DOMAIN 221 327 CH3.
 FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 27 83 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 141 201
 FT DISULFID 247 305
 SQ SEQUENCE 327 AA; 35940 MW; 3EDBD81EF208E7A CRC64;

Query Match 37.18; Score 50.5; DB 1; Length 327;
 Best Local Similarity 42.38; Pred. No. 4.6;
 Matches 11; Conservative 7; Mismatches 7; Indels 1; Gaps 1;

OY 1 CRTTHPLPKDIYRSTAKAPG-RAP 25
 DB 201 CKVSKGLSPSSIEKTSKAGQPREP 226

RESULT 11
 ID GC4_MOUSE STANDARD: PRT; 330 AA.
 AC P01863;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Ig gamma-2a chain C region, A allele.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RP SEQUENCE FROM N.A.
 RP MEDLINE=81076554; PubMed=6777755;
 RA Sikorav J.-L., Aufray C., Rougeon F.;
 RT "Structure of the constant and 3' untranslated regions of the murine
 RL Balb/c gamma 2a heavy chain messenger RNA.";
 RL Nucleic Acids Res. 8:3143-3155(1980).
 RN [2]
 RP SEQUENCE FROM N.A.
 RP MEDLINE=81198976; PubMed=6262729;
 RA Yamawaki-Kataoka Y., Miyata T., Honjo T.;
 RT "The complete nucleotide sequence of mouse immunoglobulin gamma 2a gene
 RT and evolution of heavy chain genes: further evidence for intervening
 RL sequence-mediated domain transfer.";
 RL Nucleic Acids Res. 9:1365-1381(1981).
 RN [3]
 RP SEQUENCE FROM N.A.
 RP MEDLINE=81223894; PubMed=6787604;
 RA O'Lo R., Aufray C., Morchamps C., Rougeon F.;
 RT "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes
 RT suggests that exons can be exchanged between genes in a multigenic
 RL family.";
 RL Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).
 RN [4]
 RP MYELOMA PROTEIN MOPC 173.
 RP MEDLINE=74175517; PubMed=4831970;
 RA Bourgois A., Fougerau M., Rocca-Serra J.;

RT *Determination of the primary structure of a mouse IgG2a
 RT immunoglobulin: amino acid sequence of the Fc fragment. Implications
 RT for the evolution of immunoglobulin structure and function.";
 RL Eur. J. Biochem. 43:423-435(1974).
 RN [5]
 RP DISULFIDE BONDS.
 RX MEDLINE=73056887; PubMed=4565406;
 RA de Preval C., Fougereau M.;
 RT "Determination of the primary structure of a mouse gamma G2a
 RT immunoglobulin. Identification of the disulfide bridges.";
 RL Eur. J. Biochem. 30:452-462(1972).
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 CC -----
 CC DR EMBL; V00798; CAA24178.1; -
 DR PIR; A02152; G2MSA.
 DR HSSP; P01842; 7FAB.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003597; Ig_c1.
 DR InterPro: IPR003600; Ig_like.
 DR Pfam; PF00047; Ig_3.
 DR SMART; SM00410; Ig_Like; 1.
 DR SMART; SM00407; IgC1; 2.
 DR PROSITE; PS00290; Ig_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1 1
 FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 27 82
 FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 144 204
 FT DISULFID 250 308
 FT DISULFID 330 330
 FT MOD_RES 330 330
 SQ SEQUENCE 330 AA; 36389 MW; B84361C545A6864 CRC64;
 REMOVED POST-TRANSLATIONALLV.
 Query Match 37.1%; Score 50.5; DB 1; Length 330;
 Best Local Similarity 46.2%; Pred. No. 4.7;
 Matches 12; Conservative 4; Mismatches 9; Indels 1; Gaps 1;
 QY 1 CRVTHPHLPKDIYRSIAKAPG-RAP 25
 ID GCAM_MOUSE STANDARD; PRT; 399 AA.
 AC P01865;
 DT 21-JUL-1986 (rel. 01, Created)
 DT 01-AUG-1991 (rel. 19, Last sequence update)
 DT 15-JUL-1999 (rel. 38, Last annotation update)
 DE Ig gamma-2A chain C region, membrane-bound form.
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8222190; PubMed=6283537;
 RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
 RT "Nucleotide sequences of gene segments encoding membrane domains of
 RT immunoglobulin gamma chains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
 CC -I- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
 CC SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED

CC GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
 CC BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
 CC IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
 CC SEGMENT OF MU CHAINS.
 CC -I- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 1-329 IS ASSUMED TO BE
 CC IDENTICAL WITH THE CORRESPONDING REGION OF THE SECRETED FORM OF
 CC THE A ALLELE.
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 CC -----
 CC DR EMBL; J00471; AAB59661.1; ALT_INIT.
 DR PIR; A02154; G2MSAM.
 DR HSSP; P01857; 1FC1.
 DR MGD; MGI:96443; Igh-1.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003597; Ig_c1.
 DR InterPro: IPR003600; Ig_like.
 DR Pfam; PF00047; Ig_3.
 DR SMART; SM00410; Ig_Like; 1.
 DR SMART; SM00407; IgC1; 2.
 DR PROSITE; PS00290; Ig_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW Transmembrane; Alternative splicing.
 FT NON_TER 1 1
 FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 27 82
 FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 144 204
 FT DISULFID 250 308
 FT TRANSMEM 346 363
 FT POTENTIAL. CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 364 399
 FT CARBOHYD 180 180 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 399 AA; 44020 MW; 4C38138BFAED3FE0 CRC64;
 Query Match 37.1%; Score 50.5; DB 1; Length 399;
 Best Local Similarity 46.2%; Pred. No. 5.7;
 Matches 12; Conservative 4; Mismatches 9; Indels 1; Gaps 1;
 QY 1 CRVTHPHLPKDIYRSIAKAPG-RAP 25
 ID MYH7_RABIT STANDARD; PRT; 736 AA.
 AC P04461;
 DT 13-AUG-1987 (rel. 05, Created)
 DT 13-AUG-1987 (rel. 05, Last sequence update)
 DT 16-OCT-2001 (rel. 40, Last annotation update)
 DE Myosin heavy chain, cardiac muscle beta isoform (MYHC-beta) (Beta
 DE isomyosin) (fragment).
 GN MYH7.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Heart ventricle;
 RX MEDLINE=84135762; PubMed=6321481;
 RA Kavinsky C.J., Umeda P.K., Levin J.E., Sinha A.M., Nigro J.M.,
 RA Jakovics S., Rabnowitz M.;
 RT "Analysis of cloned mRNA sequences encoding subfragment 2 and part of

RT subfragment 1 of alpha- and beta-myosin heavy chains of rabbit heart." ;

RL J. Biol. Chem. 259:2775-2781(1984).

RN [2]

RX SEQUENCE OF 458-544 FROM N.A.

RN MEDLINE=84221901; PubMed=6328491;

RA Friedman D.J., Umeda P.K., Sinha A.M., Hsu H.J., Jakovcic S., Rabinowitz M.;

RT "Characterization of genomic clones specifying rabbit alpha- and beta-ventricular myosin heavy chains." ;

RL Proc. Natl. Acad. Sci. U.S.A. 81:3044-3048(1984).

RN [3]

RX SEQUENCE OF 600-720 FROM N.A.

RN MEDLINE=83299886; PubMed=6193509;

RA Sinha A.M., Umeda P.K., Kavinsky C.J., Rajamanickam C., Hsu H.J., Jakovcic S., Rabinowitz M.;

RT "Molecular cloning of mRNA sequences for cardiac alpha- and beta-form myosin heavy chains: expression in ventricles of normal, hypothyroid, and thyrotoxic rabbits." ;

RL Proc. Natl. Acad. Sci. U.S.A. 79:5847-5851(1982).

CC -1- FUNCTION: MUSCLE CONTRACTION.

CC -1- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC) AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2)

CC -1- SUBCELLULAR LOCATION: thick filaments of the myofibrils.

CC -1- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

CC -1- PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

CC -1- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LM) AND 1 HEAVY MEROMYOSIN (HM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED SUBFRAGMENT (S2).

CC -1- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.

CC -1- SIMILARITY: CONTAINS 1 IQ DOMAIN.

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CC -----

DR EMBL: K02444; AAA1414.1; -

DR EMBL: K01696; AAA31417.1; -

DR EMBL: J00672; AAA31413.1; -

DR PIR: A02987; MWRGB.

DR HSSP: P08799; 1MMN.

DR InterPro: IPR000048; IQ.

DR InterPro: IPR002928; Myosin_tail.

DR InterPro: IPR001609; Myosin_head.

DR Pfam: PF00612; IQ; 2.

DR Pfam: PF00063; myosin_head; 1.

DR Pfam: PF01576; Myosin_tail; 1.

DR ProDom: PD000355; myosin_head; 1.

DR SMART: SM00015; IQ; 1.

DR PROSITE: PS50096; IQ; 1.

KW Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding; ATP-binding; Methylation; Alkylation; Multigene family;

KW Calmodulin-binding.

FT NON_TER 1 344 MYOSIN HEAD-LIKE.

FT DOMAIN 345 374 IQ.

FT DOMAIN 403 >736 COILED COIL (POPEPITAL).

FT MOD_RES 259 259 ALKYLATION (SH-1).

FT MOD_RES 269 269 ALKYLATION (SH-2).

FT NON_TER 736 736

SQ SEQUENCE 736 AA; 85432 MW; 37DBBD7A4B6DEC43 CRC64;

Query Match 36.8%; Score 50; DB 1; Length 736;

Best Local Similarity 45.0%; Pred. No. 12; Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Oy 2 RYTHPLPDIYRSIAKAPG 21

Db 227 RSTHPHFVRCIIPNETKSPG 246

RESULT 14

MYH7_MESAU STANDARD; PRT; 1934 AA.

AC P13540; Q60540;

DT 01-JAN-1990 (Rel. 13, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Myosin heavy chain, cardiac muscle beta isoform (MYHC-beta).

GN MYH7.

OS Mesocricetus auratus (Golden hamster).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Mesocricetus.

OX NCBI_TaxID=10036;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Flb; TISSUE=Liver;

RX MEDLINE=95115033; PubMed=7815459;

RA Wang R., Sole M.J., Cukerman E., Liew C.-C.;

RT "Characterization and nucleotide sequence of the cardiac alpha-myosin heavy chain gene from Syrian hamster." ;

RL J. Mol. Cell. Cardiol. 26:1155-1165(1994).

RN [2]

RP SEQUENCE OF 962-1935 FROM N.A.

RX MEDLINE=88247788; PubMed=3380703;

RA Jendreski M.A., Sole M.J., Liew C.-C.;

RT "Sequence of cDNA encoding the Syrian hamster cardiac beta-myosin heavy chain." ;

RL Nucleic Acids Res. 16:4737-4737(1988).

CC -1- FUNCTION: MUSCLE CONTRACTION.

CC -1- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC) AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

CC -1- SUBCELLULAR LOCATION: thick filaments of the myofibrils.

CC -1- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

CC -1- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LM) AND 1 HEAVY MEROMYOSIN (HM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED SUBFRAGMENT (S2).

CC -1- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.

CC -1- SIMILARITY: CONTAINS 1 IQ DOMAIN.

CC -----

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CC -----

DR EMBL: L12104; AA62313.1; -

DR EMBL: X07273; CA30256.1; -

DR PIR: A28298; A28298.

DR HSSP: P08799; 1MMD.

DR InterPro: IPR000048; IQ.

DR InterPro: IPR004009; Myosin_N.

DR InterPro: IPR002928; Myosin_tail.

DR InterPro: IPR001609; myosin_head.

DR Pfam: PF00612; IQ; 2.

DR Pfam: PF00063; myosin_head; 1.

DR Pfam: PF02736; Myosin_N; 1.

DR Pfam: PF01576; Myosin_tail; 1.

DR PRINTS: PR00193; MYOSINHEAVY.

DR ProDom: PD000355; myosin_head: 1.
 DR SMART: SM00015; IQ: 1.
 DR SMART: SM00242; MYSC: 1.
 DR PROSITE: PS50096; IQ: 1.
 KM ATP-binding; Myosin protein; Coiled coil; Thick filament; Actin-binding;
 KM ATP-binding; Myosin protein; Coiled coil; Thick filament; Actin-binding;
 KM Calmodulin-binding; Alkylation; Multigene family;
 FT DOMAIN 1 779 MYOSIN HEAD-LIKE.
 FT DOMAIN 809 IQ.
 FT DOMAIN 839 1934 COILED COIL (POTENTIAL).
 FT NP_BIND 177 184 APP.
 FT DOMAIN 654 676 ACTIN-BINDING.
 FT DOMAIN 756 770 ACTIN-BINDING.
 FT MOD_RES 128 128 METHYLATION (TR-1) (POTENTIAL).
 FT MOD_RES 694 694 ALKYLATION (SH-1) (POTENTIAL).
 FT MOD_RES 704 704 ALKYLATION (SH-2) (POTENTIAL).
 FT CONFLICT 966 966 D -> E (IN REF. 2).
 FT CONFLICT 978 978 T -> TE (IN REF. 2).
 FT CONFLICT 986 986 E -> Q (IN REF. 2).
 FT CONFLICT 1008 1014 DLADED -> ALAKRT (IN REF. 2).
 FT CONFLICT 1057 1057 D -> Y (IN REF. 2).
 FT CONFLICT 1060 1060 L -> V (IN REF. 2).
 FT CONFLICT 1095 1095 D -> N (IN REF. 2).
 FT CONFLICT 1217 1217 E -> D (IN REF. 2).
 FT CONFLICT 1271 1271 D -> N (IN REF. 2).
 FT CONFLICT 1327 1327 T -> A (IN REF. 2).
 FT CONFLICT 1358 1358 C -> R (IN REF. 2).
 FT CONFLICT 1504 1504 L -> V (IN REF. 2).
 FT CONFLICT 1537 1537 M -> L (IN REF. 2).
 FT CONFLICT 1556 1556 N -> K (IN REF. 2).
 SQ SEQUENCE 1934 AA; 222928 MW; FDBAG58310BDB57D CRC64;

Query Match 36.8%; Score 50; DB 1; Length 1934;
 Best Local Similarity 45.0%; Pred. No. 33;
 Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 2 RYHPPHLPDIYRIAKAPG 21
 ID | | | | | : : : : : | : |
 DB 662 RSTHPPHRCITIPNETKSPG 681

RESULT 15
 MYH7_HUMAN STANDARD; PRT; 1935 AA.
 AC P12883; O14904; O16579;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Myosin heavy chain, cardiac muscle beta isoform (MYHC-beta).
 GN MYH7 OR MYHCB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91065634; PubMed=2249844;
 RA Jelenicki T., Diederich K.W., Haas W., Schleich J., Iachter P.,
 RA Pfister M., Bach A., Vosberg H.P.;
 RT "The complete sequence of the human beta-myosin heavy chain gene and
 RT a comparative analysis of its product.";
 RL Genomics 8:194-206(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90301496; PubMed=2362820;
 RA Liew C.-C., Sole M.J., Yamauchi-Takahara K., Kellam B.,
 RA Anderson D.H., Lin L., Liew J.;
 RT "Complete sequence and organization of the human cardiac beta-myosin
 RT heavy chain gene.";
 RL Nucleic Acids Res. 18:3647-3651(1990).
 RN [3]
 RP SEQUENCE OF 1-115 FROM N.A.

RX MEDLINE=89264452; PubMed=2726733;
 RA Yamauchi-Takahara K., Sole M.J., Liew J., Ing D., Liew C.-C.;
 RT "Characterization of human cardiac myosin heavy chain genes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:3504-3508(1989).
 RN [4]
 RP ERRATUM.
 RA Yamauchi-Takahara K., Sole M.J., Liew J., Ing D., Liew C.-C.;
 RL Proc. Natl. Acad. Sci. U.S.A. 86:7416-7417(1989).
 RN [5]
 RP SEQUENCE OF 1310-1935 FROM N.A.
 RX MEDLINE=86176778; PubMed=2421254;
 RA Saez L., Liewand L.A.;
 RT "Characterization of diverse forms of myosin heavy chain expressed in
 RT adult human skeletal muscle.";
 RL Nucleic Acids Res. 14:2951-2969(1986).
 RN [6]
 RP REVISTONS.
 RA Liewand L.A.;
 RL Submitted (MAR-1988) to the EMBL/Genbank/DBJ databases.
 RN [7]
 RP SEQUENCE OF 1410-1935 FROM N.A.
 RX MEDLINE=88299163; PubMed=2969919;
 RA Kurabayashi M., Tsuchimochi H., Komuro I., Takaku F., Yazaki Y.;
 RT "Molecular cloning and characterization of human cardiac alpha- and
 RT beta-form myosin heavy chain complementary DNA clones. Regulation of
 RT expression during development and pressure overload in human
 RT atriium.";
 RL J. Clin. Invest. 82:524-531(1988).
 RN [8]
 RP SEQUENCE OF 785-1935 FROM N.A.
 RX TISSUE-Skeletal muscle;
 RC MEDLINE=90235862; PubMed=1691980;
 RA Bober E., Buchberger-Seidl A., Braun T., Singh S., Goedde H.W.,
 RA Arnold H.H.;
 RT "Identification of three developmentally controlled isoforms of human
 RT myosin heavy chains.";
 RL Eur. J. Biochem. 189:55-65(1990).
 RN [9]
 RP SEQUENCE OF 1393-1935 FROM N.A.
 RX MEDLINE=87192738; PubMed=3032769;
 RA Jandreski M.A., Liew C.-C.;
 RT "Construction of a human ventricular cDNA library and
 RT characterization of a beta myosin heavy chain cDNA clone.";
 RL Hum. Genet. 76:47-53(1987).
 RN [10]
 RP REVIEW ON VARIANTS.
 RX MEDLINE=96039076; PubMed=8533830;
 RA Arai S., Matsuoaka R., Hirayama K., Sukurai H., Tamura M., Ozawa T.,
 RA Kimura M., Imamura S.-I., Furutani Y., Joh-O K., Kawana M., Takao A.,
 RA Hosoda S., Momma K.;
 RT "Missense mutation of the beta-cardiac myosin heavy-chain gene in
 RT hypertrophic cardiomyopathy.";
 RL Am. J. Med. Genet. 58:267-276(1995).
 RN [11]
 RP VARIANTS CMH1 GLU-256 AND ARG-741.
 RX MEDLINE=93248216; PubMed=8483915;
 RA Pananapazir L., Dalakas M.C., Cyran F., Cohn G., Epstein N.D.;
 RT "Missense mutations in the beta-myosin heavy-chain gene cause central
 RT core disease in hypertrophic cardiomyopathy.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:3993-3997(1993).
 RN [12]
 RP VARIANT CMH1 GLN-403.
 RX MEDLINE=90367131; PubMed=1975517;
 RA Gelsterfer-Lowrance A.A.T., Kass S., Tanigawa G., Vosberg H.-P.,
 RA McKenna W., Seidman C.E., Seidman J.G.;
 RT "A molecular basis for familial hypertrophic cardiomyopathy: a beta
 RT cardiac myosin heavy chain gene missense mutation.";
 RL Cell 62:999-1006(1990).
 RN [13]
 RP VARIANTS CMH1 GLN-249, GLN-403, CYS-453 AND MET-606.
 RX MEDLINE=92204193; PubMed=1552912;
 RA Watkins H., Rosenzweig A., Hwang D.S., Levi T., McKenna W.,
 RA Seidmann C.E., Seidmann J.G.;

RT "Characteristics and prognostic implications of myosin missense
 RT mutations in familial hypertrophic cardiomyopathy.";
 RL New Engl. J. Med. 326:1108-1114(1992).
 RN [14]
 RP VARIANTS CMH1 GLN-403: CYS-453, ARG-584 AND MET-606.
 RX MEDLINE-94070863; PubMed-8250038;
 RA Watkins H., Thierfelder L., Anan R., Jarcho J., Matsumori A.,
 McKenna W., Seidman J.G., Seidman C.E.;
 RT "Independent origin of identical beta cardiac myosin heavy-chain
 RT mutations in hypertrophic cardiomyopathy.";
 RL Am. J. Hum. Genet. 53:1180-1185(1993).
 RN [15]
 RP VARIANTS CMH1 GLN-403 AND VAL-908.
 RX MEDLINE-92346810; PubMed-1638703;
 RA Epstein N.D., Cohn G.M., Gyran F., Fananapazir L.;
 RT "Differences in clinical expression of hypertrophic cardiomyopathy
 RT associated with two distinct mutations in the beta-myosin heavy chain
 RT gene. A 908Leu->Val mutation and a 403Arg->Gln mutation.";
 RL Circulation 86:345-352(1992).
 RN [16]
 RP VARIANTS CMH1 LEU-403 AND TRP-403.
 RX MEDLINE-94075629; PubMed-8254035;
 RA Dausse E., Komajda M., Feltier L., Dubourg O., Dufour C., Carrier L.,
 Wisniewsky C., Bercevic J., Hengstenberg C., Al-Mahdawi S.,
 RT "Familial hypertrophic cardiomyopathy. Microsatellite haplotyping and
 RT identification of a hot spot for mutations in the beta-myosin heavy
 RT chain gene.";
 RL J. Clin. Invest. 92:2807-2813(1993).
 RN [17]
 RP VARIANTS CMH1 TRP-403.
 RX MEDLINE-94093568; PubMed-8268932;
 RA Woolmen J.C., Brink P.A., Corfield V.A.;
 RT "Identification of a new missense mutation at Arg403, a Cpg mutation
 RT hotspot, in exon 13 of the beta-myosin heavy chain gene in
 RT hypertrophic cardiomyopathy.";
 RL Hum. Mol. Genet. 2:1731-1732(1993).
 RN [18]
 RP VARIANTS CMH1 ASN-615.
 RX MEDLINE-93038688; PubMed-1417858;
 RA Nishi H., Kimura A., Harada H., Toshima H., Sasazuki T.;
 RT "Novel missense mutation in cardiac beta myosin heavy chain gene
 RT found in a Japanese patient with hypertrophic cardiomyopathy.";
 RL Biochem. Biophys. Res. Commun. 188:379-387(1992).
 RN [19]
 RP VARIANTS CMH1 GLY-778.
 RX MEDLINE-93343938; PubMed-8343162;
 RA Harada H., Kimura A., Nishi H., Sasazuki T., Toshima H.;
 RT "A missense mutation of cardiac beta-myosin heavy chain gene linked
 RT to familial hypertrophic cardiomyopathy in affected Japanese
 RT families.";
 RL Biochem. Biophys. Res. Commun. 194:791-798(1993).
 RN [20]
 RP VARIANTS CMH1 VAL-908.
 RX MEDLINE-93168485; PubMed-8435239;
 RA Al-Mahdawi S., Chamberlain S., Cleland J., Nihoyannopoulos P.,
 Gilligan D., French J., Choudhury L., Williamson R., Oakley C.;
 RT "Identification of a mutation in the beta cardiac myosin heavy chain
 RT gene in a family with hypertrophic cardiomyopathy.";
 RL Br. Heart J. 69:136-141(1993).
 RN [21]
 RP VARIANTS CMH1 TRP-719.
 RX MEDLINE-95179132; PubMed-7874131;
 RA Greve G., Bachinski L., Friedman D.L., Czernuszewicz G., Anan R.,
 Towbin J., Seidman C.E., Roberts R.;
 RT "Isolation of a de novo mutant myocardial beta MHC protein in a
 RT pedigree with hypertrophic cardiomyopathy.";
 RL Hum. Mol. Genet. 3:2073-2075(1994).
 RN [22]
 RP VARIANTS CMH1 CYS-513: ARG-716 AND TRP-719.
 RX MEDLINE-94110336; PubMed-8282798;
 RA Anan R., Greve G., Thierfelder L., Watkins H., McKenna W., Solomon S.,
 Vecchio C., Shono H., Nakao S., Tanaka H., Mares A. Jr., Towbin J.A.,
 Spillio R., Roberts R., Seidman J.G., Seidman C.E.;

RT "Prognostic implications of novel beta cardiac myosin heavy chain gene
 RT mutations that cause familial hypertrophic cardiomyopathy.";
 RL J. Clin. Invest. 93:280-285(1994).
 RN [23]
 RP VARIANTS CMH1 THR-797.
 RX MEDLINE-96047159; PubMed-7581410;
 RA Woolmen J.C., Brink P.A., Corfield V.A.;
 RT "Identification of a novel Ala797Thr mutation in exon 21 of the beta-
 RT myosin heavy chain gene in hypertrophic cardiomyopathy.";
 RL Hum. Mutat. 6:197-198(1995).
 RN [24]
 RP VARIANTS CMH1 CYS-453.
 RX MEDLINE-96209901; PubMed-8655135;
 RA Ko Y.-L., Chen J.-D., Tang T.-K., Cheng J.-D., Lin S.-Y., Liou Y.-C.,
 RA Kuan P., Wu C.-W., Lien W.-P., Liew C.-C.;
 RT "Malignant familial hypertrophic cardiomyopathy in a family with a
 RT 453Arg->Cys mutation in the beta-myosin heavy chain gene:
 RT coexistence of sudden death and end-stage heart failure.";
 RL Hum. Genet. 97:585-590(1996).
 RN [25]
 RP VARIANTS CMH1 THR-349 AND TRP-719.
 RX MEDLINE-98204402; PubMed-9544842;
 RA Jeschke B., Uhl K., Weist B., Schroder D., Weidinger T.,
 RA Dohlemann C., Vosberg H.-P.;
 RT "A high risk phenotype of hypertrophic cardiomyopathy associated with

Query Match 36.8%; Score 50; DB 1; Length 1935;
 Best Local Similarity 45.0%; Pred. NO. 33;
 Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
 QY 2 RYTHPLPKDIVRSIAKAP 21
 DB 663 RSTHPHFVRCILPNETKSPG 682

Search completed: July 15, 2002, 12:49:43
 Job time: 204 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 15, 2002, 12:45:44 ; Search time 25.08 Seconds
(without alignments)
172.443 Million cell updates/sec

Title: US-09-938-700-4

Sequence: 1 CRYTHPHLPDVRISAKAPGRAP 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 100%

Listing first 45 summaries

Database :

1: SPREMBL.19:*
2: sp.archaea:*
3: sp.bacteria:*
4: sp.fungi:*
5: sp.human:*
6: sp.invertebrate:*
7: sp.mammal:*
8: sp.mhc:*
9: sp.organelle:*
10: sp.phage:*
11: sp.plant:*
12: sp.todent:*
13: sp.virus:*
14: sp.vertibrate:*
15: sp.unclassified:*
16: sp.virus:*
17: sp.bacteriap:*
17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Query Length | DB ID | Description |
|------------|-------|-------|--------------|-------|-------------|
| 1 | 59 | 43.4 | 684 | 13 | Q90544 |
| 2 | 54 | 39.7 | 99 | 6 | Q9MWS5 |
| 3 | 52 | 38.2 | 273 | 16 | Q9ANR3 |
| 4 | 51 | 37.3 | 197 | 2 | Q9ZB8 |
| 5 | 50.5 | 37.1 | 538 | 16 | Q9R9R8 |
| 6 | 50 | 36.8 | 68 | 4 | Q9DUM8 |
| 7 | 50 | 36.8 | 797 | 6 | Q9T5U6 |
| 8 | 50 | 36.8 | 1038 | 6 | Q28699 |
| 9 | 50 | 36.8 | 1935 | 6 | Q9HID5 |
| 10 | 50 | 36.8 | 1935 | 6 | Q9GKR1 |
| 11 | 50 | 36.8 | 1935 | 6 | Q9BR39 |
| 12 | 50 | 36.8 | 1935 | 11 | Q91Z83 |
| 13 | 49.5 | 36.4 | 468 | 11 | Q9GL31 |
| 14 | 49.5 | 36.4 | 473 | 11 | Q9YL25 |
| 15 | 49.5 | 36.4 | 473 | 11 | Q91Z05 |
| 16 | 49 | 36.0 | 840 | 13 | Q91BN3 |

| | | | | | | |
|----|------|------|------|----|--------|-----------------------|
| 17 | 49 | 36.0 | 1598 | 11 | Q922D2 | Q922D2 mus musculus |
| 18 | 49 | 36.0 | 1937 | 6 | Q9TV62 | Q9TV62 sus scrofa |
| 19 | 49 | 36.0 | 1938 | 6 | Q9BE40 | Q9BE40 bos taurus |
| 20 | 49 | 36.0 | 1939 | 6 | Q9TV63 | Q9TV63 sus scrofa |
| 21 | 49 | 36.0 | 1939 | 6 | Q9TV61 | Q9TV61 sus scrofa |
| 22 | 49 | 36.0 | 1939 | 13 | Q9PTV2 | Q9PTV2 gallus galli |
| 23 | 49 | 36.0 | 1940 | 6 | Q9BE41 | Q9BE41 bos taurus |
| 24 | 49 | 36.0 | 1941 | 13 | Q9DGM4 | Q9DGM4 gallus galli |
| 25 | 49 | 36.0 | 1944 | 13 | Q9YEL5 | Q9YEL5 aegypium p |
| 26 | 48.5 | 35.7 | 1944 | 17 | Q9YEL5 | Q9YEL5 mus musculus |
| 27 | 48.5 | 35.7 | 504 | 11 | Q9BOM4 | Q9BOM4 caenorhabditis |
| 28 | 48.5 | 35.7 | 660 | 5 | Q23573 | Q23573 homo sapien |
| 29 | 48.5 | 35.7 | 701 | 4 | Q96P08 | Q96P08 equus caball |
| 30 | 48 | 35.3 | 337 | 6 | Q95M34 | Q95M34 equus caball |
| 31 | 48 | 35.3 | 460 | 5 | Q9V7W8 | Q9V7W8 rattus norv |
| 32 | 48 | 35.3 | 753 | 11 | Q9JHW8 | Q9JHW8 rattus norv |
| 33 | 48 | 35.3 | 804 | 4 | Q9UPQ3 | Q9UPQ3 homo sapien |
| 34 | 48 | 35.3 | 855 | 16 | Q53900 | Q53900 mycobacteri |
| 35 | 48 | 35.3 | 875 | 4 | Q96RK3 | Q96RK3 homo sapien |
| 36 | 48 | 35.3 | 876 | 4 | Q96P47 | Q96P47 homo sapien |
| 37 | 48 | 35.3 | 979 | 12 | Q9DVU0 | Q9DVU0 pluteella xy |
| 38 | 48 | 35.3 | 1191 | 2 | Q52484 | Q52484 serripa ma |
| 39 | 48 | 35.3 | 1287 | 13 | Q93498 | Q93498 theragra ch |
| 40 | 48 | 35.3 | 1929 | 13 | Q98T06 | Q98T06 notonthena |
| 41 | 48 | 35.3 | 1930 | 13 | Q9PGD5 | Q9PGD5 pennaria ar |
| 42 | 48 | 35.3 | 1931 | 13 | Q42352 | Q42352 cyprinus ca |
| 43 | 48 | 35.3 | 1932 | 13 | Q98T04 | Q98T04 notonthena |
| 44 | 48 | 35.3 | 1933 | 13 | Q90337 | Q90337 cyprinus ca |
| 45 | 48 | 35.3 | 1935 | 13 | Q902E5 | Q902E5 brachydanio |

ALIGNMENTS

| RESULT | 1 | PRELIMINARY: | PRT: | 684 AA. |
|--------|--|--------------|------|---------|
| ID | Q90544 | | | |
| AC | Q90544 | | | |
| DT | 01-NOV-1996 (TREMBL) | | | |
| DT | 01-NOV-1996 (TREMBL) | | | |
| DT | 01-DEC-2001 (TREMBL) | | | |
| DE | NOVEL ANTIGEN RECEPTOR PRECURSOR. | | | |
| OS | Ginglymstoma cirratum (Nurse shark). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes; | | | |
| OC | Elaeobranchii; Galeomorphi; Galeoidea; Orectolobiformes; | | | |
| OC | Ginglymstomatidae; Ginglymstoma. | | | |
| OX | NCBI_TaxID=7801; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | TISUE=SPLEEN; | | | |
| RX | MEDLINE=95183140; PubMed=7877689; | | | |
| RA | Greenberg A.S., Avila D., Hughes M., Hughes E.C., | | | |
| RA | Plajnik M.F.; | | | |
| RT | "A new antigen receptor gene family that undergoes rearrangement and | | | |
| RT | extensive somatic diversification in sharks."; | | | |
| RL | Nature 374:168-173(1995). | | | |
| DR | EMBL: U18701; A048195.1; - | | | |
| DR | HSSP: P01709; ZWCG. | | | |
| DR | Interpro: IPR003597; Ig-cl. | | | |
| DR | Interpro: IPR003600; Ig-like. | | | |
| DR | Interpro: IPR003006; Ig_MHC. | | | |
| DR | Pfam: PF00047; Ig; 6. | | | |
| DR | SMART: SM00407; IgC1; 4. | | | |
| DR | SMART: SM00410; IgC1; 2. | | | |
| DR | PROSITE: PS00290; Ig_MHC; UNKNOWN_3. | | | |
| KW | SIGNAL: Receptor. | | | |
| FT | SIGNAL | | | |
| FT | CHAIN | | | |
| FT | SEQUENCE | | | |
| FT | 684 AA; 75224 MW; 2EP9D2071CDA6DFD CRC64; | | | |

Query Match 43.4%; Score 59; DB 13; Length 684;
Best Local Similarity 50.0%; Pred. No. 2.4;

Matches 11; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRVTHPLPKDIVRSIAKAPCK 22
 ||| |::| |::| |
 Db 645 CLVGHPSLNRDLIRSRKSNCK 666

RESULT 2

Q9K9R8

PRELIMINARY; PRT; 99 AA.

AC Q9K9R8; PRELIMINARY; PRT; 99 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DE MYOSIN HEAVY CHAIN (FRAGMENT).

GN MYH6.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI_TaxID=9986;

RN [1]

RC SEQUENCE FROM N.A.

RP STRAIN-NEW ZEALAND WHITE; TISSUE=HEART;

RA Sayeed R.A., Grace A.A., Vandenberg J.I.;

RT "Patterns of ion channel expression in cardiac hypertrophy."

RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ291317; CAB94849.1; -

DR HSP; P13538; 2MTS.

DR InterPro: IPR001609; myosin_head.

DR Pfam: PF00063; myosin_head; 1.

DR Prodom: PD000355; myosin_head; 1.

FT NON_TER 1 1

FT SEQUENCE 99 AA; 10933 MW; 3961CA1047DB2E0C CRC64;

SQ

Query Match 39.7%; Score 54; DB 6; Length 99;
 Best Local Similarity 50.0%; Pred. No. 1.7;
 Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 2 RVTHPLPKDIVRSIAKAPK 21
 ||| |::| |::| |
 Db 79 RTHPHFVRCILIRPKRANG 98

RESULT 3

Q9AAN3

PRELIMINARY; PRT; 273 AA.

AC Q9AAN3; PRELIMINARY; PRT; 273 AA.

DT 01-JUN-2001 (TREMBLrel. 17, Created)

DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DE HYPOTHETICAL PROTEIN CC0564.

GN CC0564.

OS Caulobacter crescentus.

OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;

OC Caulobacter.

OX NCBI_TaxID=69394;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-ATCC 19089 / CB15;

RA MEDLIN=21173698; PubMed=11259647;

RA Elsen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

RA Deboy R.T., Dodson R.J., Durkin A.S., Gwin M.L., Haft D.H.,

RA Kolony J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

RA Ullrich T., Tran K., Wolf A., Vamatheva M., Shetty J., Berry K.,

RA Salberg S.L., Venter J.C., Shapiro L., Fraser C.M.,

RA "Complete genome sequence of Caulobacter crescentus."

RT Pfoc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

DL EMBL; AB005730; AKK22550.1; -

DR TIGR; CC0564; -

KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 273 AA; 29461 MW; C1C6D2F87E432082 CRC64;

Query Match 38.2%; Score 52; DB 16; Length 273;
 Best Local Similarity 40.6%; Pred. No. 9.7;
 Matches 13; Conservative 5; Mismatches 4; Indels 10; Gaps 2;

QY 4 TRPHLP--KDIVRS-----IAKAPGRAP 25
 ||| |::| |::| |
 Db 224 SRPHAPNRDLIRSLTGLGRPLCARANGRRAP 255

RESULT 4

Q9ZBJ8

PRELIMINARY; PRT; 197 AA.

AC Q9ZBJ8; PRELIMINARY; PRT; 197 AA.

DT 01-MAY-1999 (TREMBLrel. 10, Created)

DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)

DE HYPOTHETICAL 21.1 KDA PROTEIN.

GN SC9C7.12.

OS Streptomyces coelicolor.

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.

OX NCBI_TaxID=1902;

RN [1]

RC SEQUENCE FROM N.A.

RP STRAIN-A3(2);

RA Seeger K.J., Harris D.;

RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ035161; CAA22724.1; -

DR MOL. Microbiol. 21:77-96(1996).

DR "A set of ordered cosmid and a detailed genetic and physical map for

DR the 8 Mb Streptomyces coelicolor A3(2) chromosome."

DR HYPOTHETICAL protein.

SQ SEQUENCE 197 AA; 21061 MW; 6ABC3643C5570AC1 CRC64;

KW

Query Match 37.5%; Score 51; DB 2; Length 197;
 Best Local Similarity 42.9%; Pred. No. 9.7;
 Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 3 VTHPLPKDIVRSIAKAPCK 23
 ||| |::| |::| |
 Db 177 LAHPALQAARVALAKIRPGR 197

RESULT 5

Q9K9R8

PRELIMINARY; PRT; 538 AA.

AC Q9K9R8; PRELIMINARY; PRT; 538 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DE BH2577 PROTEIN.

GN BH2577.

OS Bacillus halodurans.

OC Bacteria; Firmicutes; Bacillus/Clostridium group;

OC Bacillus/Staphylococcus group; Bacillus.

OX NCBI_TaxID=86665;

RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-C-125 / JCM 9153;
 RX MEDLINE-20512582; PubMed-11058132;
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
 RA Fujii F., Hirama C., Nakamura Y., Ogasawara N., Kubota S.,
 RA Horikoshi K.;
 RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
 RT halodurans and genomic sequence comparison with Bacillus subtilis.";
 RL Nucleic Acids Res. 28:4317-4331(2000).
 DR EMBL: AF001516; BAB06296.1; -
 KW Complete proteome.
 SO SEQUENCE 538 AA; 62270 MW; 470E31DE2FC0C507 CRC64;

Query Match 37.1%; Score 50.5; DB 16; Length 538;
 Best Local Similarity 41.7%; Pred. No. 33;
 Matches 10; Conservative 4; Mismatches 9; Indels 1; Gaps 1;

OY 2 RYTHPLP-KDIVRSIAKAPGKRA 24
 DB 431 QIRSHKPKIDLAQIGETGKLA 454

RESULT 6
 OYUM8 PRELIMINARY; PRT; 68 AA.
 AC 09UM8;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE BETA-MYOSIN HEAVY CHAIN (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-89154425; PubMed-2522082;
 RA Diederich K.W., Eisele I., Ried T., Jaenicke T., Lichter P.,
 RA Vosberg H.P.;
 RT "Isolation and characterization of the complete human beta-myosin
 RT heavy chain gene.";
 RL Hum. Genet. 81:214-220(1989).
 DR EMBL: M27636; AAF9019.1; -
 DR HSSP: P13538; 2MXS.
 DR InterPro: IPR001609; myosin_head.
 DR Pfam: PF00063; myosin_head.1.
 DR ProDom: PD000355; myosin_head.1.
 DR NON_TER 1
 FT NON_TER 68
 FT SEQUENCE 68 AA; 7890 MW; B58C9D8951B4D1C2 CRC64;

Query Match 36.8%; Score 50; DB 4; Length 68;
 Best Local Similarity 45.0%; Pred. No. 4.5;
 Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 2 RYTHPLP-KDIVRSIAKAPG 21
 DB 11 RSTHPRFRCILIPNETKSPG 30

RESULT 7
 ID 09TSU6 PRELIMINARY; PRT; 797 AA.
 AC 09TSU6;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE BETA MYOSIN HEAVY CHAIN (FRAGMENT).
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.

OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-20353874; PubMed-10895319;
 RA Meurs K.M., Kittleson M., Spangler E., Ware W.A., Womack J.E.,
 RA Townin J.A.;
 RT "Nine polymorphisms within the head and hinge region of the feline
 RT cardiac beta-myosin heavy chain gene.";
 RL Ann. Genet. 31:231-231(2000).
 DR EMBL: AF008572; AAD51477.1; -
 DR EMBL: U93854; AAD51477.1; JOINED.
 DR EMBL: AF001618; AAD51477.1; JOINED.
 DR EMBL: AF001619; AAD51477.1; JOINED.
 DR EMBL: AF002811; AAD51477.1; JOINED.
 DR EMBL: AF002812; AAD51477.1; JOINED.
 DR EMBL: AF002813; AAD51477.1; JOINED.
 DR EMBL: AF003767; AAD51477.1; JOINED.
 DR EMBL: AF005406; AAD51477.1; JOINED.
 DR EMBL: AF005407; AAD51477.1; JOINED.
 DR EMBL: AF005408; AAD51477.1; JOINED.
 DR EMBL: AF005409; AAD51477.1; JOINED.
 DR EMBL: AF005410; AAD51477.1; JOINED.
 DR EMBL: AF005411; AAD51477.1; JOINED.
 DR EMBL: AF005412; AAD51477.1; JOINED.
 DR EMBL: AF008570; AAD51477.1; JOINED.
 DR EMBL: AF008571; AAD51477.1; JOINED.
 DR HSSP: P08799; 1MND.
 DR InterPro: IPR000048; IO.
 DR InterPro: IPR001609; myosin_head.
 DR InterPro: IPR000533; Tropomyosin.
 DR Pfam: PF00612; IQ; 2.
 DR Pfam: PF00063; myosin_head.1.
 DR PRINTS: PR00193; MYOSINHEAVY.
 DR PRINTS: PR00194; TROPOMYOSIN.
 DR ProDom: PD000355; myosin_head.1.
 DR SMART: SM00045; IQS; 1.
 DR SMART: SM00242; MSC; 1.
 DR PROSITE: PS50096; IQ; 1.
 DR NON_TER 1
 FT NON_TER 797
 FT SEQUENCE 797 AA; 91530 MW; 60DD585187328C34 CRC64;

Query Match 36.8%; Score 50; DB 6; Length 797;
 Best Local Similarity 45.0%; Pred. No. 59;
 Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 2 RYTHPLP-KDIVRSIAKAPG 21
 DB 486 RSTHPRFRCILIPNETKSPG 505

RESULT 8
 ID 028699 PRELIMINARY; PRT; 1038 AA.
 AC 028699;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE BETA CARDIAC MYOSIN HEAVY CHAIN (FRAGMENT).
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-SKELETAL MUSCLE;
 RA Jaenicke T., Goldspink G.,
 RT "unpublished.";
 RL submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE OF 57-809 FROM N.A.
 RC TISSUE-SKELETAL MUSCLE;

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RX MEDLINE=64135762; PubMed=6321481;
RA Kavanisky C.V., Umeda P.K., Levin J.E., Sinha A.M., Nigro J.M.,
RA Jakovic S., Rabinowitz M.;
RT "Analysis of cloned mRNA sequences encoding subfragment 2 and part of
RT subfragment 1 of alpha- and beta-myosin heavy chains of rabbit
RT heart."
RL J. Biol. Chem. 259:2775-2781(1984).
DR EMBL: Z34886; CAAB4369.1; -.
DR HSP: P08799; IMD.
DR InterPro: IPR000048; IQ.
DR InterPro: IPR001609; myosin_head.
DR InterPro: IPR002928; myosin_tail.
DR InterPro: IPR000533; Tropomyosin.
DR Pfam: PF00612; IQ; 2.
DR Pfam: PF00063; myosin_head; 1.
DR Pfam: PF01576; myosin_tail; 1.
DR PRINTS: PR00193; MYOSINHEAVY.
DR PRINTS: PR00194; TROPOMYOSIN.
DR ProDom: PD000355; myosin_head; 1.
DR SMART: SM00015; IQ; 1.
DR PROSITE: PS50096; IQ; 1.
FT NON_TER 1 1
FT CONFLICT 123 123 O -> H (IN REF. 0,0,2 AND 1).
FT NON_TER 1038 1038
SQ SEQUENCE 1038 AA; 120160 MW; AC8A4EB34BE76A56 CRC64;

Query Match 36.8%; Score 50; DB 6; Length 1038;
Best Local Similarity 45.0%; Pred. No. 77;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 2 RVTHPHLPKDIVRSIAKAPG 21
   1 1111 : : : 1:11
Db 300 RSTHPHFVRCIIPNETKSPG 319

RESULT 9
O9HDS PRELIMINARY; PRT; 1935 AA.
AC O9HDS;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE BETA-MYOSIN HEAVY CHAIN.
GN MYH7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Wendel B., Reinhard R., Machendorf U., Zacharzowsky U.B.,
RA Osterziel K.J., Morano I., Hoche M.R.;
RT "Genomic DNA Sequence variation of the human beta-myosin heavy chain
RT gene."
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ238393; CAC20413.1; -.
DR HSP: P08799; IMD.
DR InterPro: IPR000048; IQ.
DR InterPro: IPR001609; myosin_head.
DR InterPro: IPR004009; myosin_tail.
DR InterPro: IPR002928; myosin_tail.
DR Pfam: PF00063; myosin_head; 1.
DR Pfam: PF02736; myosin_head; 1.
DR Pfam: PF01576; myosin_tail; 1.
DR PRINTS: PR00193; MYOSINHEAVY.
DR ProDom: PD000355; myosin_head; 1.
DR SMART: SM00015; IQ; 1.
DR PROSITE: PS50096; IQ; 1.
SQ SEQUENCE 1935 AA; 223100 MW; 317PD7EB277C972 CRC64;

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Query Match 36.8%; Score 50; DB 4; Length 1935;
Best Local Similarity 45.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 2 RVTHPHLPKDIVRSIAKAPG 21
   1 1111 : : : 1:11
Db 663 RSTHPHFVRCIIPNETKSPG 682

RESULT 10
O9GKR1 PRELIMINARY; PRT; 1935 AA.
AC O9GKR1;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MYOSIN HEAVY CHAIN SLOW ISOFORM.
GN MYHC-SLOW.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OC NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-LANDRACE; TISSUE-SKELETAL MUSCLE;
RA Chikuni K., Muroya S., Nakajima I.;
RT "Sequencing of the porcine myosin heavy chain slow isoform."
RL EMBL: AB052226; BAB20630.1; -.
DR HSP: P08799; IMD.
DR InterPro: IPR000048; IQ.
DR InterPro: IPR001609; myosin_head.
DR InterPro: IPR004009; myosin_tail.
DR InterPro: IPR002928; myosin_tail.
DR Pfam: PF00063; myosin_head; 1.
DR Pfam: PF02736; myosin_head; 1.
DR Pfam: PF01576; myosin_tail; 1.
DR PRINTS: PR00193; MYOSINHEAVY.
DR ProDom: PD000355; myosin_head; 1.
DR SMART: SM00015; IQ; 1.
DR SMART: SM00242; MYSC; 1.
DR PROSITE: PS50096; IQ; 1.
SQ SEQUENCE 1935 AA; 223297 MW; 270556D9A3B86C4A CRC64;

Query Match 36.8%; Score 50; DB 6; Length 1935;
Best Local Similarity 45.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 2 RVTHPHLPKDIVRSIAKAPG 21
   1 1111 : : : 1:11
Db 663 RSTHPHFVRCIIPNETKSPG 682

RESULT 11
O9BE39 PRELIMINARY; PRT; 1935 AA.
AC O9BE39;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MYOSIN HEAVY CHAIN SLOW.
GN MYHC-SLOW.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-HOLSTEIN; TISSUE-SKELETAL MUSCLE;
RA Chikuni K., Muroya S., Nakajima I.;
RT "Sequencing of the bovine myosin heavy chain isoforms."

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RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB059400; BAB40922.1; -
 DR HSSP: P08799; 1MND
 DR InterPro: IPR000046; IQ
 DR InterPro: IPR001609; myosin_head
 DR InterPro: IPR004009; myosin_N
 DR InterPro: IPR002928; myosin_tail
 DR Pfam: PF00063; myosin_head.1
 DR Pfam: PF02736; myosin_N.1
 DR Pfam: PF01576; myosin_tail.1
 DR PRINTS: PR00193; MYOSINHEAVY
 DR PRODOM: PD000355; myosin_head.1
 DR SMART: SM00015; IQ.1
 DR SMART: SM00242; MYSC.1
 DR PROSITE: PS50096; IQ.1
 SQ SEQUENCE 1935 AA; 223228 MW; DEA05200BCFA2557 CRC64;

Query Match 36.8%; Score 50; DB 6; Length 1935;
 Best Local Similarity 45.0%; Pred. No. 1.5e+02;
 Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 2 RVTHPHLPKDIVRSIAKAPG 21
 1 1111 : : : 1:11
 DB 663 RSTHPHFVRCILPNETKSPG 682

RESULT 12
 O91283 PRELIMINARY; PRT; 1935 AA.
 AC O91283;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE BETA MYOSIN HEAVY CHAIN.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB;
 RA Gulick J.D., Robbins J.;
 RT "In Vivo Examination of Myosin Heavy Chain Isoform Functionality in
 the Heart."
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY056464; AAL17913.1; -
 DR SEQUENCE 1935 AA; 222878 MW; 08CDD03573B10CF0 CRC64;

Query Match 36.8%; Score 50; DB 11; Length 1935;
 Best Local Similarity 45.0%; Pred. No. 1.5e+02;
 Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 2 RVTHPHLPKDIVRSIAKAPG 21
 1 1111 : : : 1:11
 DB 663 RSTHPHFVRCILPNETKSPG 682

RESULT 13
 O99131 PRELIMINARY; PRT; 468 AA.
 AC O99131;
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC003878; AAH03878.1; -
 DR HSSP: P01842; 7FAB.
 DR InterPro: IPR003597; IQ
 DR InterPro: IPR003597; IQ.cl
 DR InterPro: IPR003600; IQ_1ike
 DR InterPro: IPR003066; IQ_MHC.
 DR InterPro: IPR003596; IQ_V.
 DR Pfam: PF00047; IQ.4
 DR SMART: SM00409; IQ.2
 DR SMART: SM00407; IQcl.3
 DR SMART: SM00406; IGV.1
 DR SMART: SM00410; IQ_1ike.1
 DR PROSITE: PS00290; IQ_MHC; UNKNOWN.1
 SQ SEQUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;

Query Match 36.4%; Score 49.5; DB 11; Length 468;
 Best Local Similarity 46.2%; Pred. No. 40;
 Matches 12; Conservative 4; Mismatches 9; Indels 1; Gaps 1;

OY 1 CRVTHPHLPKDIVRSIAKAPG-RAP 25
 1 : : 11 : : : 1 : 111
 DB 342 CKVNNKALPAPIERTISKPGSVRAP 367

RESULT 14
 O99125 PRELIMINARY; PRT; 473 AA.
 AC O99125;
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Strausberg R.;
 RA Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC003888; AAH03888.1; -
 DR HSSP: P01842; 7FAB.
 DR InterPro: IPR003597; IQ
 DR InterPro: IPR003597; IQ.cl
 DR InterPro: IPR003600; IQ_1ike
 DR InterPro: IPR003066; IQ_MHC.
 DR InterPro: IPR003596; IQ_V.
 DR Pfam: PF00047; IQ.4
 DR SMART: SM00409; IQ.2
 DR SMART: SM00407; IQcl.3
 DR SMART: SM00406; IGV.1
 DR SMART: SM00410; IQ_1ike.1
 DR PROSITE: PS00290; IQ_MHC; UNKNOWN.1
 SQ SEQUENCE 473 AA; 52449 MW; BE9869B7986DA155 CRC64;

Query Match 36.4%; Score 49.5; DB 11; Length 473;
 Best Local Similarity 46.2%; Pred. No. 40;
 Matches 12; Conservative 4; Mismatches 9; Indels 1; Gaps 1;

OY 1 CRVTHPHLPKDIVRSIAKAPG-RAP 25
 1 : : 11 : : : 1 : 111
 DB 347 CKVNNKALPAPIERTISKPGSVRAP 372

RESULT 15
 O91205 PRELIMINARY; PRT; 473 AA.
 AC O91205;
 DT 01-DEC-2001 (TREMblrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DR 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE HYPOTHEETICAL, 51.9 KDA PROTEIN.
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 NC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 OX NM_1_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC010327; AAI10327.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 473 AA; 51946 MW; CE625F008932AF12 CRC64;

| | | | | |
|-----------------------|----------------|-------------------------------|----------|------------|
| Query Match | 36.4% | Score 49.5 | DB 11 | Length 473 |
| Best Local Similarity | 46.2% | Pred. No. 40 | | |
| Matches 12 | Conservative 4 | Mismatches 9 | Indels 1 | Gaps 1 |
| QY | 1 | CRVTHPHLPKDIYRSIAKAPG-KRAP 25 | | |
| | 1:1:1 | 1:1:1 | 1:1:1 | 1:1:1 |
| DB | 347 | CRVNNKDPSPFIERTISKGLVAP 372 | | |

Search completed: July 15, 2002, 12:49:27
Job time: 223 sec